

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1835	100.0	1835	6	BC011962	Sequence	
2	1569.4	85.5	1790	9	BC042674	Homo sapi	
3	1362	74.2	4377	6	AX492941	Sequence	
4	1337.2	72.9	3648	6	AX417817	Sequence	
5	996.4	54.3	4612	4	OCPPHLIP	Z12841 O. cuniculus	
6	889	48.4	4608	10	AF045454	Cavia por	
7	805.2	43.9	4590	10	D63648	D63648 Rattus nor	
8	805.2	43.9	4613	6	E13935	E13935 Rat mRNA fo	
c 9	575	31.3	583	6	AX417820	Sequence	
10	466	25.4	1776	6	CQ175991	Sequence	
c 11	440.2	24.0	446	6	AX417823	Sequence	
12	411	22.4	43543	6	AX417864	Sequence	
13	411	22.4	180465	9	AC074011	Homo sapi	
14	381.6	20.8	163595	2	AC022076	Homo sapi	
15	322.2	17.6	820	10	BC033606	Mus muscu	
16	241.2	13.1	3565	9	BC065041	Homo sapi	
17	236	12.9	265	6	AX417822	Sequence	
18	188.6	10.3	608	6	AX417821	Sequence	
19	186.8	10.2	2477	6	AX417306	Sequence	

AUTHORS **JOURNAL**

Strausberg, R.
Direct Submission
Submitted (02-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK **COMMENT**

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg6bcm.tmc.edu
Gunsatne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.O., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 50 Row: k Column: 10.

FEATURES **source**

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/note="Vector: pCMV-SPORT6"

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CDS

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ORIGIN

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Best Local Similarity 93.5%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 1; Indels 117; Gaps 2;

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Db	49	GCCCAAGAGTCTGTGTAACCTCGTGGACTTCTCGAACCCTCATCATCGGCGAGGTGT	108
Qy	131	CCTGGGAAACCCACACAAGTSCCAGTGCAGAGCGGCGGAGCATGCGCGAGCTGGT	190

Db	109	CTTGGGAAACCCACACAAGTSCCAGTGCAGAGCGCA-----	146
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Db	147	-----	146
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Qy	371	CGGAATAGTAACTACAGTACCCCATCAAGCCAGCCATTGGAAGACTGGGGCAGTGACTTC	430
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Qy	431	CTGTGTACAGAGTGAAGGCTTCCAATAGTGTTCACACCTCTGTCCACAGCTCCGACCA	490
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Qy	491	GCAGACATCAAAAGTGTGGCGCCCTGGGTGACTCTCTGACTACAGCATGGGAGCTCGA	550
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Qy	731	GGGSCCAGAGCTAGGGACATGCCAGCCAGCCCTGGGACCTGTTAGAGCGAATGAAAAAC	790
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Db	1024	ACACAGCGTGAAGACTTTGGGTTGTGGTGGAGCTTTCTTCCAAAACACACTCACCCCA	1083
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Qy	1451	GCCCCGAGGTGCTCTACTGGGCTGTCCAGTGGCAGCGGGAGTGGGCTGTGGTGGGC	1510
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Db	1444	AGCTGCGCATGTGGCCCTCTAGCCCGGGGGTGGGTCTCAACCTAACTCCCTATAG	1503
Qy	1631	CCACTCTCTTCAACCGCCCTCTGCGCCAGCCACTCCCGGCCACAGGACATGCTTCAATGC	1690
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Qy	1751	GCCTATGCTCTCTGGAATGATACATTTAAATTAAGTCCAAAGCTATTTTAAAAA	1810
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Db	1684	AAAAAAAAAAAAAAAAAAAAA	1708
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LOCUS	Sequence 1 from Patent WO02059328.		
DEFINITION	AX492941		
ACCESSION	AX492941.1	GI:23338611	
VERSION			
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	Turner Jr, C.A., Miranda, M. and Yu, X.		
AUTHORS	Human lipase and polynucleotides encoding the same		
TITLE	Patent: WO 02059328-A 1 01-AUG-2002;		
JOURNAL	LEXICON GENETICS INC (US)		
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Best Local Similarity	89.3%;	Pred. No. 0;	
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QY 1323 CAGTGGGCGGCAAGACTACCTTCCAACTTCAACCCACAGCCGAGCCAACTCAAGTGC 1382
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QY 1383 CCTCTCTGAGAGCCCTTACTCTACACCTTGGGACAGCCGATTTGCTCCAGACCAGG 1442
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QY 1443 CTGAAGAGCCCGAGGTGCTTACTGGGCTGTCCAGTGGCAGCGGAGTGGCCCTTG 1502
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RESULT 4
AX417817
LOCUS AX417817 3648 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 1 from Patent WO0231161.
ACCESSION AX417817
VERSION AX417817.1 GI:21522937

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 Zhu, Z.

AUTHORS Regulation of human phospholipase-like enzyme

TITLE Patent: WO 0231161-A 1 18-APR-2002;

JOURNAL BAYER AG (DE)

FEATURES Location/Qualifiers

source 1..3648

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ORIGIN

Query Match 72.9%; Score 1337.2; DB 6; Length 3648;
Best Local Similarity 88.8%; Pred. No. 0;
Matches 1562; Conservative 0; Mismatches 8; Indels 190; Gaps 3;
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QY 61 TCCCTTAGGTGCCAGAGTCTTGTCAACCTCGTGGAGTTCCTTCAACCCCACTATCATGC 120
Db 1955 -----AGGTGCCAGAGTCTTGTCAACCTCGTGGAGTTCCTTCAACCCCACTATCATGC 2008
QY 121 GGCAGGTGTTCTCTGGGAAACCCAGACAAAGTGCAGTGCAGCAGGCCA----- 168
Db 2009 GGCAGGTGTTCTCTGGGAAACCCAGACAAAGTGCAGTGCAGCAGGCCA----- 2068
QY 169 ----- 168
Db 2069 ACTGCGTTTGAACCTCGGGGAGAACTCCCAAGAGCTAGCCAGGCTGGAGGCTTTCAGCC 2128
QY 169 -----GAGCAGCATGCGAGCTGTGGGTGAGGCTGAGCGCGTATGACACGAGAGG 218
Db 2129 GAGCTTACCGGAGCATGCGGAGCTGTGGGTGAGGCTGAGCGCGTATGACACGAGAGG 2188
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QY 274 ----- 273
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Qy 1111 CCACATGGCATCTCCAGTTCTCTCTACTGCGACCAATACACAGCGTGGAGCTTTGC 1170
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Qy 1765 AATGATACATTTAAATAA 1784
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RESULT 6
AF045454
LOCUS AF045454 4608 bp mRNA linear ROD 02-JUN-1998
DEFINITION Cavia porcellus phospholipase B (PLB) mRNA, complete cds.
ACCESSION AF045454
VERSION AF045454.1 GI:3172336
KEYWORDS
SOURCE Cavia porcellus (domestic guinea pig)
ORGANISM Cavia porcellus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
REFERENCE 1 (bases 1 to 4608)
AUTHORS Delagebeaudeuf, C., Gassama-Diagne, A., Nauze, M., Ragab, A., Li, R.Y.,
Capdevielle, J., Ferrara, P., Fauvel, J. and Chap, H.
TITLE Ectopic epididymal expression of guinea pig intestinal
phospholipase B. Possible role in sperm maturation and activation
by limited proteolytic digestion
J. Biol. Chem. 273 (22), 13407-13414 (1998)
JOURNAL 98256256
MEDLINE 9593672
PUBMED
REFERENCE 2 (bases 1 to 4608)
AUTHORS Delagebeaudeuf, C., Gassama-Diagne, A., Nauze, M., Ragab, A., Li, R.Y.,
Capdevielle, J., Ferrara, P., Fauvel, J. and Chap, H.
TITLE Direct Submission
JOURNAL Submitted (30-JAN-1998) INSERM unite 326, Hopital Purpan, Toulouse
31059, France
FEATURES
source
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40. 4431
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Qy	1288	GATGGCCATCGCACTCTGGAAACACATCTGGAACAGTGGCGGCAAGACTACTCTCAA	1347
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Qy	1634	CTCTTCTTACCGGCTCTGCGCCAGCCACTCCCGGCGCAGGACATGCTTCAATGCTCTG	1693
Db	4470	CCCTCTTCAACAGTCCCTCTCTCGGTGACACAGGAGCCAAACGAGCTATTGTGACTTCTG	4529
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Db	4530	G 4530	
RESULT 7			
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DEFINITION	D63648		
ACCESSION	D63648.1	GI:2696235	
VERSION			
KEYWORDS		phospholipase B.	
SOURCE		Rattus norvegicus (Norway rat)	
ORGANISM		Rattus norvegicus	
REFERENCE		1 (sites)	
AUTHORS		Takenori, H., Zolotarov, F. N., Ting, L., Urbain, T., Komatsubara, T.,	
TITLE		Hatanaka, O., Okamoto, M. and Tojo, H.	
JOURNAL		Identification of functional domains of rat intestinal	
MEDLINE		phospholipase B/lipase. Its cDNA cloning, expression, and tissue	
PUBMED		distribution	
REFERENCE		J. Biol. Chem. 273 (4), 2222-2231 (1998)	
AUTHORS		2 (bases 1 to 4590)	
TITLE		Direct Submission	
JOURNAL		Submitted (22-JUL-1995) Hiromasa Tojo, Osaka University Medical	
MEDLINE		School, Molecular Physiological Chemistry; 2-2 Yamada-oka, Suita,	
PUBMED		Osaka 565, Japan (E-mail: htojo@mr-bio.med.osaka-u.ac.jp,	
REFERENCE		Tel: 06-879-3283 (ex. 3283), Fax: 06-879-3288)	
AUTHORS		Location/Qualifiers	
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Db	3704	TCCGGAGAACTACTCAACACAGGAGTATGTCAAGATACATCCAGCATGCCCTTGGACATCTT	3763			
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Db	3764	CTATGAGGAGCTTCCACAGGTTTTTCATCAACGTGGTGGAAAGTCAATGAGAGCTGTCCGGTCT	3823			
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Db	3824	GCTCCACGACACGGCGGGGAAATGTGCCATGCTGGCTTGGCTGTCCAGAAAAAATGCACTTG	3883			
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Db	3884	CCTTAAACGCTCTCAAAACCTCATGCGCAATGACAGGAGCTGAAGAAAGTCAACGGGAACCT	3943			
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Db	4244	TGTCGGGAACAGTCAAGATTCTTCTAGACAAAGGTAAAGAAAACTCCAATACACTCTACTG	4303			
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RESULT 8						
E13935						
LOCUS	E13935 4613 bp DNA linear PAT 27-APR-1998					
DEFINITION	Rat mRNA for phospholipase.					
ACCESSION	E13935					
VERSION	E13935.1 GI:3252702					
KEYWORDS	JP 1997248190-A/1.					
SOURCE	Rattus sp.					
ORGANISM	Rattus sp.					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;						
Rattus.						
REFERENCE	1 (bases 1 to 4613)					
AUTHORS	Tojo, H. and Hasegawa, A.					
TITLE	NEW PHOSPHOLIPASE AND DNA CODING THE SAME					
JOURNAL	Patent: JP 1997248190-A 1 22-SEP-1997;					
TOJO HIROMASA, TONEN CORP						
COMMENT	OS Rattus sp. (rat)					
	PN JP 1997248190-A/1					

[illegible]


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Db 583 AGAGAGGGGACACTGACCTCTCTCTCTCCGAGGACTGTTTCACTTCTCAGACCGCG 524
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Db 523 GGCATGCGGAGATGGCCATCGCACTCTTGGAACAACATGCTGGAACCAAGTGGCGCGCAAGA 464
Qy 1338 CTACCTCTCAACAACATTTCAACCCACAGCGAGCAAACTCAAGTGGCCCTCTCTCTGAGAGCC 1397
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Db 163 CTTCACTGCTCTTGCAGCCACTCCCGSCACAGGACATGCTTCAATGCTGGTGC 104
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RESULT 10
LOCUS CQ715991 1776 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 1925 from Patent WO02068579.
ACCESSION CQ715991
VERSION CQ715991.1 GI:42276848
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kts, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 1925 06-SEP-2002; PE Corporation (NY) (US)
FEATURES source
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Best Local Similarity 100.0%; Pred. No. 3.3e-107;
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1491 CAACATCTCTGGAACCAAGTGGCGCGCAAGACTTACCTCTCAACAACTTCAACCCACAGCCGAGC 1550
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Qy 1489 GGGAGTGGGCTTGTGGTGGCATCATCGGACAGTGGTCTTGGAGGTGCGAGGAGGTGG 1548
Db 1671 GGGAGTGGGCTTGTGGTGGCATCATCGGACAGTGGTCTTGGAGGTGCGAGGAGGTGG 1730
Qy 1549 CCGAGGGAAGATCTCTCAATGAGCCTGCGCACTGTGGCCCTCTAG 1594
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RESULT 11
LOCUS AX417823/c 446 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 7 from Patent WO0231161.
ACCESSION AX417823
VERSION AX417823.1 GI:21522941
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Zhu, Z.
TITLE Regulation of human phospholipase-like enzyme
JOURNAL Patent: WO 0231161-A 7 18-APR-2002; BAYER AG (DE)
FEATURES source
Location/Qualifiers
1. .446
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 24.0%; Score 440.2; DB 6; Length 446;
Best Local Similarity 99.1%; Pred. No. 9.5e-101;
Matches 442; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1355 ACCCAGACGCGAGCCAAACTCAAGTGCCTCTCTCTGAGAGCCCTTACCTCTACACCTG 1414
Db 446 ACCCAGACGCGAGCCAAACTCAAGTGCCTCTCTCTGAGAGCCCTTACCTCTACACCTG 387
Qy 1415 CGGAACAGCCGATTTGCTCCAGACAGGCTGGAAGAGCCCGAGGTGCTTACTGGGCT 1474
Db 386 CGGAACAGCCGATTTGCTCCAGACAGGCTGGAAGAGCCCGAGGTGCTTACTGGGCT 327
Qy 1475 GTCCAGTGGCAGCGGAGTGGCCCTTGTGGGATCATCGGACAGTGGTCTGAGG 1534
Db 326 GTCCAGTGGCAGCGGAGTGGCCCTTGTGGGATCATCGGACAGTGGTCTGAGG 267
Qy 1535 TGCAGAGAGGTGCGCGGAGGAAGATCTTCCAAATGAGCCTGCGCACTGTGGCCCTCTAG 1594
Db 266 TGCAGAGAGGTGCGCGGAGGAAGATCTTCCAAATGAGCCTGCGCACTGTGGCCCTCTAG 207
Qy 1595 GCCCGGGGGTGGTCTCTCAACCTTAACTCCCTATAGCCACTCTCTTCCAGCCCTCTGCC 1654
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Mon Mar 28 09:43:23 2005

Db 206 GCGCGGGGTGGTCTCTACCTTAACCTCCCTATAGCCACCTCTTTCACCGCCCTCTGCC 147

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Db 146 CCAGCCACTCCCGGCCACAGACATGCTTCAATGCTGGTGCCTATAGACCCAGGG 87

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Db 26 TTTAAATAAAGTCCAAAGCTATTITA 1

RESULT 12

AX711964 43543 bp DNA linear PAT 10-APR-2003

DEFINITION Sequence 3 from Patent WO02062977.

ACCESSION AX711964

VERSION AX711964.1 GI:29787749

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Yan, C., Ketchum, K., di Francesco, V. and Beasley, E.M.

TITLE Human phospholipase B-like polypeptide and uses thereof

JOURNAL Patent: WO 02062977-A 3 13-AUG-2002;

PE Corporation (NY) (US)

FEATURES

Location/Qualifiers

1. 43543

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 22.4%; Score 411; DB 6; Length 43543;

Best Local Similarity 98.8%; Pred. No. 6.1e-93;

Matches 414; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy 1442 GCTGAAGAGAGCCCGGAGGTCTCTACTGGGCTGTCCAGTGGCAGCGGAGTGGGCTT 1501

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Db 41246 GTGGTGGGATCATCGGACAGTGTCTGAGGTGCGAGAGTGGCGGAGGAGAT 41305

Qy 1562 CCTCCATGAGCTGCGACTGTGGCCCTCTAGGCGCGGGGTGGGTCTTCACTTAAC 1621

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Db 41366 TCCTATAGCCACTCTTTCACCGCCCTGTGCCCGCCAGCCTCCCGGCCACAGGACATG 41425

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Qy 1742 TTCTTCCAGGCTATGCTCTCTGGAATGATACATTTAAATAGTCCAAAGCTATTITA 1800

Db 41486 TTCTTCCAGGCTATGCTCTCTGGAATGATACATTTAAATAGTCCAAAGCTATTITA 41544

RESULT 13

AC074011

LOCUS

DEFINITION Homo sapiens BAC clone RP11-780J6 from 2, complete sequence.

ACCESSION AC074011

VERSION AC074011.5 GI:15144519

KEYWORDS

SOURCE HTG.

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Sulston, J.E. and Waterston, R.

TITLE Toward a complete human genome sequence

JOURNAL Genome Res. 8 (11), 1097-1108 (1998)

REFERENCE 99063792

MEDLINE 9847074

REFERENCE 2 (bases 1 to 180465)

AUTHORS Paulson, B., Cotton, M. and Lohmeyer, A.

TITLE The sequence of Homo sapiens BAC clone RP11-780J6

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 180465)

AUTHORS Waterston, R.H.

JOURNAL Direct Submission

REFERENCE 4 (bases 1 to 180465)

AUTHORS Submitted (09-JUL-2000) Genome Sequencing Center, Washington University School of Medicine, 444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 5 (bases 1 to 180465)

AUTHORS Waterston, R.

JOURNAL Direct Submission

REFERENCE 6 (bases 1 to 180465)

AUTHORS Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT On Aug 9, 2001 this sequence version replaced gi:13431259.

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: sapiens@watson.wustl.edu

----- Summary Statistics -----

Center project name: H_NH0780J06

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION: The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenos, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute

(http://bacpac.med.buffalo.edu)

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is AC022076. Actual start of this clone is at base position 1 of RP11-780J6; actual end is at base position 180465 of RP11-780J6.

FEATURES

source

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/chromosome="2"

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/clone_lib="RPCI-11"

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repeat_region

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repeat_region

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repeat_region

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repeat_region 35626. .35687

Query Match 22.4%; Score 411; DB 9; Length 180465;

Best Local Similarity 98.8%; Pred. No. 7.9e-93;

Matches 414; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1382 CCTCTCCTGAGAGCCCTTACCTCTACACCTCGGGAACAGCCGATGCTCCAGACAG 1441
Db 102291 CCTCCACAGGAGAGCCCTTACCTCTACACCTCGGGAACAGCCGATGCTCCAGACAG 102350
Qy 1442 GCTGAGAGAGCCCGAGGCTGCTTACTGGGCTGTCCAGTGGCAGGAGTGGGCTT 1501
Db 102351 GCTGAGAGAGCCCGAGGCTGCTTACTGGGCTGTCCAGTGGCAGGAGTGGGCTT 102410
Qy 1502 GTGGTGGGCATCATCGGACAGTGGTCTGAGAGTGCAGGAGAGGTGGCCGAGGGAAGAT 1561
Db 102411 GTGGTGGGCATCATCGGACAGTGGTCTGAGAGTGCAGGAGAGGTGGCCGAGGGAAGAT 102470
Qy 1562 CCTCCAATGAGCCTGCGCACTGTGGCCCTCTAGGCCCGGGGTGGGTCTCACCCCTAAAC 1621

Mon Mar 28 09:43:23 2005

TITLE
JOURNAL

Direct Submission
Submitted (26-JAN-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 163595)
Worley, K.C.
Direct Submission
Submitted (08-JAN-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Apr 28, 2002 this sequence version replaced gi:16117882.

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

102471 CCTCCATAGGCTGGCCACTTGGCCCTCTAGGCCCGGGGGTGGTCTCACCTAAAC 102530
1622 TCCTATAGCACTCTTTCACCGCCCTCTGCCCGCCAGCCACTCCCGGCCACGACATG 1681
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RESULT 14

AC022076 163595 bp DNA linear HTG 08-JAN-2003
LOCUS Homo sapiens chromosome 3 clone RP11-34L7, WORKING DRAFT SEQUENCE,
DEFINITION 11 unordered pieces.

AC022076
VERSION AC022076.13 GI:20335454

KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo..

REFERENCE

AUTHORS

1 (bases 1 to 163595)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Albrow, S.L., Amaral, H.C., Are, J.R., Ayale, M., Banks, T.,
Barbata, J., Benton, J., Blum, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brice, M., Brown, E., Brown, M., Bryant, N.P.,
Buck, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthett, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Earhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlik, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hogue, M., Holloway, C., Hollins, B.,
Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsso, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulsaged, H.,
Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Metzger, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Mosier, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenwo, S., Oguh, M., Okwuonu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peary, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G.,
Scherv, S., Scott, G., Shen, H., Shoshitari, N., Sisson, I.,
Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Tang, H.,
Tutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Thomas, S.,
Tansley, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Ugmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williams, A., Wleczky, R., Woodson, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G., and Gibbs, R.

TITLE

JOURNAL

REFERENCE

AUTHORS

ORIGIN

Query Match 20.8%; Score 381.6; DB 2; Length 163595;
Best Local Similarity 97.1%; Pred. No. 2.4e-85;
Matches 409; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

FEATURES
source

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/db_xref="taxon:9606"
/chromosome="3"
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NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 11 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

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2570 2669: gap of unknown length
2670 4826: contig of 2157 bp in length
4827 4926: gap of unknown length
4927 8967: contig of 4041 bp in length
8968 9067: gap of unknown length
9068 12664: gap of unknown length
12665 17841: contig of 5077 bp in length
17842 17941: gap of unknown length
17942 27703: contig of 9762 bp in length
27704 27803: gap of unknown length
27804 38654: contig of 10851 bp in length
38655 38754: gap of unknown length
38755 50187: contig of 11433 bp in length
50188 50287: gap of unknown length
50288 60306: contig of 10019 bp in length
60307 60406: gap of unknown length
60407 84011: contig of 23604 bp in length
84011 163595: contig of 79485 bp in length.

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QY 1620 ACTCCCTATAGCCTCTTTCACCGCCCTCTAGGCCCGGGGTGGGTCTTCACTTAA 1679
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RESULT 15
LOCUS BC033606
DEFINITION Mus musculus cDNA sequence BC033606, mRNA (cDNA clone MGC:40917 IMAGE:5373588), complete cds.

ACCESSION BC033606
VERSION BC033606.1 GI:21706929

KEYWORDS MGC.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 820)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Males, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smalios, D.E., Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932

REFERENCE 2 (bases 1 to 920)
AUTHORS Director MGC Project.

Direct Submission

TITLE Submitted (02-JUL-2002) National Institutes of Health, Mammalian

JOURNAL Genome Collection (MGC), Cancer Genomics Office, National Cancer

REMARK
COMMENT

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapsb@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland,
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Hachighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Maiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W., Tauregeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 65 Row: 1 Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 26024306.

FEATURES
source

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gene

CDS

ORIGIN

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Matches 402; Conservative 0; Mismatches 133; Indels 0; Gaps 0;
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QY 1086 AACTGAGAAAGTGAACCTCGAACCTCCAGCATGCTCCAGTTTCTCTTCTGGCACC 1145
Db 101 AGCTGAAGAACTAAACTGGAACCTCCAGAGCGCATCTCCGAGCTCTCTTATTGGCACC 160
QY 1146 AATACACACAGCTGAGGACTTTGCGGTGTCGAGCCTTCTTCTTCCAAACACACTCA 1205
Db 161 GGATACATGGAGCGTGAGGACTTCGAGTCACTGTGCGACCTTTCTTCCGGAATACCTTTA 220

us-09-778-961-1.rge

Mon Mar 28 09:43:23 2005

Qy	1206	CCCACTGAACGAGAGGGGACACTGACCTCACCTTCTTCCGAGACTGTTTCACT	1265
Db	221	TCCCACTGAATGAGCGTGAGGGCTGGACCTCACTTCTTCTGAGACTGTTTCACT	280
Qy	1266	TCTCAGACCGGGGATGCGGAGATGGCCATCGCACTCTGGAACAACATGCTGGAACCAAG	1325
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Qy	1326	TGGGCGCAAGACTTACTCCAACTTCAACCAAGCGAGCCAAACTCAAGTGCCTT	1385
Db	341	TGGGCTGGAAGACATCTCTCAATACTTCATATACAAAGAACCAAACTCAAGTGCCTT	400
Qy	1386	CTCCTGAGACCCCTTACCTTACCCCTGCGGACAGCCGATTTGCTCCAGACCAAGGCTG	1445
Db	401	CACCTGAAGGCTTTTCTCTACACCCCTCGGAATAGTCAGCTTCTTCAGACCAAGGCTG	460
Qy	1446	AAGAGCCCGGAGTCTCTACTGGGCTGTCCAGTGGCAGCGGAGTCCGCCCTTGTGG	1505
Db	461	AAGAACCTTCCATGCACTCTACTGGGCACTGCGCAGTGGCAGCAATAGGTGGCTGGCAG	520
Qy	1506	TGGGCATCATCGGACACAGTGTCTGGAGGTGCGAGAGAGTGGCCGGAGGAGA	1560
Db	521	TTGGCATCTTGGAGTGAATGTTGTGAGAACTGTGAACCCGTCACACAGGAGA	575

Search completed: March 26, 2005, 22:05:21
Job time : 8030.1 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	1835	100.0	1835	6	ABQ82234	Human pho
2	1649.2	89.9	4424	8	AAD52634	Human lip
3	1627.8	88.7	4512	12	ADO19837	Human lip
4	1555.2	84.8	4607	8	AAD52626	Human lip
5	1513.8	82.5	4311	12	ADH13733	Human EN
6	1421	77.4	4425	12	ADH42430	Novel huc
7	1417.8	77.3	4425	12	ADN61816	Human cdi
8	1400	76.3	4508	12	ADO19836	Human lip
9	1374.6	74.9	4425	6	ABX97050	Human NOV
10	1362	74.2	4377	6	ABQ77623	Human lip
11	1360.4	74.1	4377	6	ABQ77624	Human lip
12	1337.2	72.9	3648	6	ABQ37410	Human pho
13	1231.8	67.1	4263	6	ABX97048	Human NOV
14	1231.8	67.1	4263	12	ADH42426	Human huc
15	1230.2	67.0	4263	12	ADN61812	Human cdi
16	805.2	43.9	4613	2	AAT91874	Rat phosph
17	667.4	36.4	802	4	AAB99765	Human pro
18	667.4	36.4	802	4	ABA08297	Human pho
19	575	31.3	583	6	ABQ37411	Human pho
20	575	31.3	583	6	ABL89761	Human pol

XX The present sequence encodes a human phospholipase protein (I) located on
CC chromosome 2. (I) can be used for identifying agents that modulate its
CC function or activity where the agent is useful for treating a disease or
CC condition mediated by a the human phospholipase protein. (I) peptides can
CC be used in substantial and specific assays related to functional
CC information of the peptide sequences, to raise antibodies or to elicit
CC immune response, as reagents in assays that determine the levels of
CC protein in biological fluids, and as markers for tissues where the
CC corresponding protein is expressed. Nucleotide sequences encoding (I) can
CC be used as probes, primers and chemical intermediates in biological
CC assays, for constructing recombinant vectors, and expressing antigenic
CC portions of the protein. (I) and nucleic acid molecules encoding it can
CC be used in the identification of therapeutic proteins and may serve as
CC models or targets for the development of human therapeutic agents that
CC modulate phospholipase activity in cells and tissues that express the
CC phospholipase, such as in kidney, blood, lung, brain glioblastomas,
CC prostate, colon or leukocytes
XX
SQ Sequence 1835 BP; 458 A; 549 C; 474 G; 354 T; 0 U; 0 Other;
Query Match 100.0%; Score 1835; DB 6; Length 1835;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1835; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGCAGCCAACTTTGTTGACCATCTCGCAATGCTTGGACGTCCTGCGATAGAGCTTT 60
DB 1 CTGCAGCCAACTTTGTTGACCATCTCGCAATGCTTGGACGTCCTGCGATAGAGCTTT 60
QY 61 TCCCTTAGTGTCCAGAGTCTGTGTAACCTCTGGACCTTCTGAAACCCCACTATCATGC 120
DB 61 TCCCTTAGTGTCCAGAGTCTGTGTAACCTCTGGACCTTCTGAAACCCCACTATCATGC 120
QY 121 GCGAGTGTCTCTGGGAAACCCAGCAAGTGCCTGAGTGCAGGCGCAGAGCATGCG 180
DB 121 GCGAGTGTCTCTGGGAAACCCAGCAAGTGCCTGAGTGCAGGCGCAGAGCATGCG 180
QY 181 CGAGTGTGGGTGAGCGCGCTATGACAGCAGGAGCTTCTCTGTGGTGTGCGAGCC 240
DB 181 CGAGTGTGGGTGAGCGCGCTATGACAGCAGGAGCTTCTCTGTGGTGTGCGAGCC 240
QY 241 CTCTTTCAGAACATCCAGCTCCCTGTCTCTGGCGCTTGAACCACTTGGAAAGCAAAACAGA 300
DB 241 CTCTTTCAGAACATCCAGCTCCCTGTCTCTGGCGCTTGAACCACTTGGAAAGCAAAACAGA 300
QY 301 GACCCCTGGAACCTGAGCAGAGATGCCCATCACTGTCCCACTCAGATGAGCCCTTCT 360
DB 301 GACCCCTGGAACCTGAGCAGAGATGCCCATCACTGTCCCACTCAGATGAGCCCTTCT 360
QY 361 GAGAACCCCTCGAATAGTACTACAGTACCCCATCAAGCCAGCCATTGAGAACTGGGG 420
DB 361 GAGAACCCCTCGAATAGTACTACAGTACCCCATCAAGCCAGCCATTGAGAACTGGGG 420
QY 421 CAGTGACTTCTGTGTACAGAGTGAAGGCTTCCCAATAGTGTTCACACTCTGTCCACCA 480
DB 421 CAGTGACTTCTGTGTACAGAGTGAAGGCTTCCCAATAGTGTTCACACTCTGTCCACCA 480
QY 481 GCTCCGACGAGCAGATCAAAAGTGTGGCGCCCTTGGTGACTCTCTGACTACAGCAGT 540
DB 481 GCTCCGACGAGCAGATCAAAAGTGTGGCGCCCTTGGTGACTCTCTGACTACAGCAGT 540
QY 541 GCGAGCTCGACCAAAACAACTCCAGTACCTACCCCATCAAGCCAGCCATTGAGAACTGGGG 600
DB 541 GCGAGCTCGACCAAAACAACTCCAGTACCTACCCCATCAAGCCAGCCATTGAGAACTGGGG 600
QY 601 CATTGGAGGGATGGGAACCTGAGACTACACACACATGCCACATCTTGAAGAGTT 660
DB 601 CATTGGAGGGATGGGAACCTGAGACTACACACACATGCCACATCTTGAAGAGTT 660
QY 661 CAACCTTACTCTCTGTGCTTCTTACAGCAGCTGGGAGGGGACAGCAGGACTAAATGT 720
DB 661 CAACCTTACTCTCTGTGCTTCTTACAGCAGCTGGGAGGGGACAGCAGGACTAAATGT 720

QY 721 GGCAGCGGAAGGGGCGCAGAGCTAGGAGCATGCGAGCCAGGCGCTGGGACCTGGTAGAGCG 780
DB 721 GGCAGCGGAAGGGGCGCAGAGCTAGGAGCATGCGAGCCAGGCGCTGGGACCTGGTAGAGCG 780
QY 781 AATGAAAAACAGCCCGGACATCAAACTGGAGAAAGACTGGAGCTGGTCAACACTTTCAT 840
DB 781 AATGAAAAACAGCCCGGACATCAAACTGGAGAAAGACTGGAGCTGGTCAACACTTTCAT 840
QY 841 TGGGGTCAACGACTTGTGTCATTACTGTGAGAAATCGGAGGCCCACTTGGCCACGGAATA 900
DB 841 TGGGGTCAACGACTTGTGTCATTACTGTGAGAAATCGGAGGCCCACTTGGCCACGGAATA 900
QY 901 TGTTCAGCAGCATCAACAGGCGCTGGACATCTCTCTGAGAGCTCCCAAGGGCTTTCG 960
DB 901 TGTTCAGCAGCATCAACAGGCGCTGGACATCTCTCTGAGAGCTCCCAAGGGCTTTCG 960
QY 961 CAACGTGTGGAGGTCTATGAGCTGTGCTACCTGTCAGGCGCAAGCGGGAATGTGC 1020
DB 961 CAACGTGTGGAGGTCTATGAGCTGTGCTACCTGTCAGGCGCAAGCGGGAATGTGC 1020
QY 1021 CATGCTGCGAGCTCAGAAACAACTGCACTTTCCTCAGACATCGCAAGCTCCCTGGAGAA 1080
DB 1021 CATGCTGCGAGCTCAGAAACAACTGCACTTTCCTCAGACATCGCAAGCTCCCTGGAGAA 1080
QY 1081 GCAAGAACTGAAGAAAGTGAACCTCCAGCATGGCATCTCCAGTTTCTCTACTG 1140
DB 1081 GCAAGAACTGAAGAAAGTGAACCTCCAGCATGGCATCTCCAGTTTCTCTACTG 1140
QY 1141 GCACCAATACACAGCGTGAAGACTTTCGCTGAGGAGCTTTCGCTGAGGAGCTTTT 1200
DB 1141 GCACCAATACACAGCGTGAAGACTTTCGCTGAGGAGCTTTCGCTGAGGAGCTTTT 1200
QY 1201 ACTCACCCTCACTGAACGAGAGGAGGACACTGACCTCCTCTCTCCGAGGAGCTTTT 1260
DB 1201 ACTCACCCTCACTGAACGAGAGGAGGACACTGACCTCCTCTCTCCGAGGAGCTTTT 1260
QY 1261 TCATTTCTCAGACCGCGGCATGCGAGATGGCCATCGCACTCTGGAACCAACATGCTGGA 1320
DB 1261 TCATTTCTCAGACCGCGGCATGCGAGATGGCCATCGCACTCTGGAACCAACATGCTGGA 1320
QY 1321 ACCAGTGGCGCGCAGAGCTACCTCCAACTTCCACCAAGCGGAGCAAACTCAAGTG 1380
DB 1321 ACCAGTGGCGCGCAGAGCTACCTCCAACTTCCACCAAGCGGAGCAAACTCAAGTG 1380
QY 1381 CCCCCTCTCTGAGAGCCCTTACCTTACACCTCGGAAACAGCGATGCTCCAGAGCA 1440
DB 1381 CCCCCTCTCTGAGAGCCCTTACCTTACACCTCGGAAACAGCGATGCTCCAGAGCA 1440
QY 1441 GGTGGAAGAGCCCGGAGTGTCTTACTGGGCTGTCCAGTGGCAGGAGTGGGCT 1500
DB 1441 GGTGGAAGAGCCCGGAGTGTCTTACTGGGCTGTCCAGTGGCAGGAGTGGGCT 1500
QY 1501 TGTGTGGGCATCATCGGACAGTGTCTGAGGTCGAGAGAGTGGCGGAGGAAAGA 1560
DB 1501 TGTGTGGGCATCATCGGACAGTGTCTGAGGTCGAGAGAGTGGCGGAGGAAAGA 1560
QY 1561 TCCTCAATGAGCTTGGCAGCTGTGCGCTCTAGGCGCGGGGTGGTCTTCACTTAA 1620
DB 1561 TCCTCAATGAGCTTGGCAGCTGTGCGCTCTAGGCGCGGGGTGGTCTTCACTTAA 1620
QY 1621 CTCCCTATAGCCACTCTTTCACCGCTCTGCCCCAGCCACTCCGGGCAACAGACAT 1680
DB 1621 CTCCCTATAGCCACTCTTTCACCGCTCTGCCCCAGCCACTCCGGGCAACAGACAT 1680
QY 1681 GCTTCAATGCTGTGTCATGGAAGCTGGAAGCTGGAAGCTGGAAGCTGGAAGCTGGA 1740
DB 1681 GCTTCAATGCTGTGTCATGGAAGCTGGAAGCTGGAAGCTGGAAGCTGGAAGCTGGA 1740
QY 1741 CTCTTCCAGGCTTATGCTCTCTGGAATGGAATACATTTAAATGCTTAAAGCTTATTTA 1800
DB 1741 CTCTTCCAGGCTTATGCTCTCTGGAATGGAATACATTTAAATGCTTAAAGCTTATTTA 1800
QY 1801 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1835

Db	1801	AA		1835
RESULT 2				
AAD52634				
ID	AAD52634	standard; cDNA; 4424 BP.		
XX	AC			
XX	AC			
XX	AC			
DT	14-MAY-2003	(first entry)		
XX				
DE	Human lipid-associated molecule (LIPAM)-9 cDNA.			
XX	Human; lipid-associated molecule; LIPAM; cardiovascular disorder; stroke;			
KW	arteriovenous fistula; atherosclerosis; hypertension; Raynaud's disease;			
KW	aneurysm; congestive heart failure; thrombophlebitis; angina pectoris;			
KW	ischemic heart disease; rheumatic heart disease; peptic oesophagitis;			
KW	gastrointestinal disorder; lipid metabolism disorder; Crohn's disease;			
KW	nausea; peptic ulcer; fatty liver; Fabry's disease; Gaucher's disease;			
KW	diabetes mellitus; hyperlipidaemia; hypercholesterolaemia; epilepsy;			
KW	autoimmune disorder; inflammatory disorder; neurological disorder; kuru;			
KW	acquired immunodeficiency syndrome; anaemia; Alzheimer's disease; asthma;			
KW	dementia; prion disease; Creutzfeldt-Jakob disease; leukaemia; cancer;			
KW	adenocarcinoma; lymphoma; melanoma; myeloma; sarcoma; gene therapy;			
protein replacement therapy; gene; es.				
XX				
OS	Homo sapiens.			
XX				
PH	Key	Location/Qualifiers		
FT	CDS	9..2918		
FT		/product= "Human LIPAM-9 protein"		
FT		/tag= a		
FT	sig_peptide	9..83		
FT		/tag= h		
FT	sig_peptide	9..74		
FT		/tag= f		
FT	sig_peptide	9..71		
FT		/tag= d		
FT	sig_peptide	9..65		
FT		/tag= b		
FT	mat_peptide	66..2915		
FT		/tag= c		
FT	mat_peptide	72..2915		
FT		/tag= e		
FT	mat_peptide	75..2915		
FT		/tag= g		
FT	mat_peptide	84..2915		
FT		/tag= i		
FT	mat_peptide			
FT		/product= "Human mature LIPAM-9 protein"		
XX				
PN	WO200294988-A2.			
XX				
XX	28-NOV-2002.			
XX				
XX	17-MAY-2002; 2002WO-US015688.			
XX				
PR	18-MAY-2001; 2001US-0292242P.			
PR	25-MAY-2001; 2001US-0293726P.			
PR	01-JUN-2001; 2001US-0295346P.			
PR	06-JUL-2001; 2001US-0303404P.			
PR	24-AUG-2001; 2001US-0314754P.			
PR	22-JAN-2002; 2002US-0351282P.			
PR	29-MAR-2002; 2002US-0368799P.			
XX	(INCY-) INCYTE GENOMICS INC.			
XX				
PI	Tang YT, Yue H, Azimzai Y, Baughn MR, Burford N, Reddy R;			
PI	Walia NK, Das D, Nguyen DB, Yao MG, Arvizu CS, Lu Y, Gandhi AR;			
PI	Griffin JA, Elliott VS, Ramkumar J, Lal PG, Lu DAM, Lee EA, Lee SY;			

PI	Yue H, Yang J, Tribouley CM, Kable AE, Swarnakar A;			
XX	WPI; 2003-120797/11.			
DR	P-PSDB; AAE34448.			
XX				
XX	New human lipid-associated molecule (LIPAM) proteins and polynucleotides,			
PT	useful for diagnosing, treating or preventing cardiovascular disorders			
PT	(e.g. aneurysms), neurological disorders (e.g. Parkinson's disease) or			
PT	cancers.			
XX				
PS	Claim 74; Page 168-169; 171pp; English.			
XX				
CC	The present invention relates to novel human lipid-associated molecules			
CC	(LIPAM) and polynucleotides encoding such proteins. Sequences of the			
CC	invention are useful for treating diseases or conditions associated with			
CC	decreased expression of functional LIPAM. The antagonist is useful for			
CC	treating a disease or condition associated with the overexpression of			
CC	functional LIPAM. They are useful for diagnosing, treating or preventing			
CC	cardiovascular disorders (e.g. arteriovenous fistula, atherosclerosis,			
CC	hypertension, Raynaud's disease, aneurysms, varicose veins, congestive			
CC	heart failure, thrombophlebitis, angina pectoris, ischaemic heart disease			
CC	or rheumatic heart disease), gastrointestinal disorders (e.g. peptic			
CC	oesophagitis, nausea, peptic ulcer or Crohn's disease), lipid metabolism			
CC	disorders (e.g. fatty liver, Fabry's disease, Gaucher's disease, diabetes			
CC	mellitus, hyperlipidaemia, hypercholesterolaemia), autoimmune disorders			
CC	or inflammatory disorders (e.g. acquired immunodeficiency syndrome,			
CC	anaemia, asthma or Crohn's disease), neurological disorders (e.g. stroke,			
CC	epilepsy, dementia, Alzheimer's disease, or prion diseases such as kuru			
CC	or Creutzfeldt-Jakob disease) or cancers (e.g. adenocarcinoma, leukaemia,			
CC	lymphoma, melanoma, myeloma or sarcoma). They are also used in gene			
CC	therapy and protein replacement therapy. The present sequence is human			
CC	LIPAM-9 cDNA			
XX				
SQ	Sequence 4424 BP; 1119 A; 1231 C; 1143 G; 931 T; 0 U; 0 Other;			
	Query Match 89.9%; Score 1649.2; DB 8; Length 4424;			
	Best Local Similarity 95.1%; Pred. No. 0;			
	Matches 1731; Conservative 0; Mismatches 68; Indels 21; Gaps 2;			
Qy	1 CTGCAGCAACTTTGTTGACCATCTCCGCAATGCTTGGAGTCTCTGCATAGAGAGCTTT 60			
Db	2626 CTGCAGCAACTTTGTTGACCATCTCCGCAATGCTTGGAGTCTCTGCATAGAG----- 2679			
Qy	61 TCCCTTAGTGCCCGAGAGTCTGTGTCACCTCTGTCGAGCTTCTCTGAACCCCACTATCATGC 120			
Db	2680 -----AGGTGCCCGAGAGTCTGTGTCACCTCTGTCGAGCTTCTCTGAACCCCACTATCATGC 2733			
Qy	121 GGACAGGTTCCTGGGAAACCCAGACAAGTCCCGAGTGCAGCAGCCGACGAGCATGCG 180			
Db	2734 GGACAGGTTCCTGGGAAACCCAGACAAGTCCCGAGTGCAGCAGCCCA-----GGA 2784			
Qy	181 CGAGCTGTGGGGTCAGGCCGCTATGACAGCAGGAGACTTCTCTGTGGTGTGCAGCC 240			
Db	2785 TGGGCTCCAGATACGTCTTCTTTGCCCGACAGCTGCATCCACCAATCAGAAATTCGA 2844			
Qy	241 CTTCTTCCAGAACATCCAGCTCCCTGTCTGGCGCTTGAACCACTTGAAGCAAAACAGA 300			
Db	2845 CTCCAGCTGGCCAGAGCCCTTTGGACCAATATGCTTTGAACCACTTGAAGCAAAACAGA 2904			
Qy	301 GACCTGGACCTGAGACGAGATGCCATCCTGTCCCACTCAGATGAGCCCTTCTCT 360			
Db	2905 GACCTGGACCTGAGACGAGATGCCATCCTGTCCCACTCAGATGAGCCCTTCTCT 2964			
Qy	361 GAGAACCCCTCGGAATAGTAACAGTACAGTACCCCATCAAGCCAGCCATTGAGAACTGGGG 420			
Db	2965 GAGAACCCCTCGGAATAGTAACAGTACAGTACCCCATCAAGCCAGCCATTGAGAACTGGGG 3024			
Qy	421 CAGTGACTTCTGTGTACAGAGTGAAGGCTTCCAATAGTGTTCACACCTCTGTCCACCA 480			
Db	3025 CAGTGACTTCTGTGTACAGAGTGAAGGCTTCCAATAGTGTTCACACCTCTGTCCACCA 3084			
Qy	481 GCTCCGACCGACAGACATCAAGTGTGGCGCCCTGGTGACTCTCTGACTACAGAGT 540			

Db	3085	GCTCCGACGACGAGACATCAAAAGTGGTGGCGCCCTCTGGTGAATCTCTGACTACAGCAGT	3144
Qy	541	GGGAGCTCGACCAAAACAACTCCAGTGACCTACCCACATCTTTGGAGGGAGCTCTCTTGGAG	600
Db	3145	GGGAGCTCGACCAAAACAACTCCAGTGACCTACCCACATCTTTGGAGGGAGCTCTCTTGGAG	3204
Qy	601	CATTGGAGGGGATGGGAATTTGAGACTCACACCACTGCGCCCACTTTGAGAGAGTT	660
Db	3205	CATTGGAGGGGATGGGAATTTGAGACTCACACCACTGCGCCCACTTTGAGAGAGTT	3264
Qy	661	CAACCTTACTCTCTGGCTTCTCTACAGACCTTGGAGGGGACAGAGAGCTAAATGT	720
Db	3265	CAACCTTACTCTCTGGCTTCTCTACAGACCTTGGAGGGGACAGAGAGCTAAATGT	3324
Qy	721	GGCAGCGGAAGGGGCCAGAGCTAGGAGCATGCCAGCCAGGGCTGGGCTGGTAGAGCG	780
Db	3325	GGCAGCGGAAGGGGCCAGAGCTAGGAGCATGCCAGCCAGGGCTGGGCTGGTAGAGCG	3384
Qy	781	AATGAAAAACAGCCCCGACATCACTGGAGAAAGACTGGAAGCTGGTCACTCTTCAAT	840
Db	3385	AATGAAAAACAGCCCCGACATCACTGGAGAAAGACTGGAAGCTGGTCACTCTTCAAT	3444
Qy	841	TGGGCTCAACGACTTGTGTCAATTAATCTGTGAATCCGGAGGCCCTTGGCCACCGAATA	900
Db	3445	TGGGCTCAACGACTTGTGTCAATTAATCTGTGAATCCGGAGGCCCTTGGCCACCGAATA	3504
Qy	901	TGTTGAGCAGATCCAGAGGCCCTTGGACATCTCTGTGAGAGCTCCCAAGGGCTTTTCT	960
Db	3505	TGTTGAGCAGATCCAGAGGCCCTTGGACATCTCTGTGAGAGCTCCCAAGGGCTTTTCT	3564
Qy	961	CAACGTGTGGAGGTCAATGAGCTGGCTAGCTCTACAGGCGGCGGAAATGTGC	1020
Db	3565	CAACGTGTGGAGGTCAATGAGCTGGCTAGCTCTACAGGCGGCGGAAATGTGC	3624
Qy	1021	CATGCTGGCAGTCAAGAACTGCACTGCTGCTGAGACCTCGAAGCTCCCTGGAGAA	1080
Db	3625	CATGCTGGCAGTCAAGAACTGCACTGCTGCTGAGACCTCGAAGCTCCCTGGAGAA	3684
Qy	1081	GAAGAACTGAAGAAAGTGAATGGAACCTCCAGATGCGATCTCTGAGTTTCTCTACTG	1140
Db	3685	GAAGAACTGAAGAAAGTGAATGGAACCTCCAGATGCGATCTCTGAGTTTCTCTACTG	3744
Qy	1141	GCAACCAATACACAGCGTGAGACTTTGGGTTGCTGGTGGAGCTTCTTCCAAAACAC	1200
Db	3745	GCAACCAATACACAGCGTGAGACTTTGGGTTGCTGGTGGAGCTTCTTCCAAAACAC	3804
Qy	1201	ACTCAGCCCACTGAACGAGAGGGGACACTGACCTTCTTCTCGAGGAGCTGTTT	1260
Db	3805	ACTCAGCCCACTGAACGAGAGGGGACACTGACCTTCTTCTCGAGGAGCTGTTT	3864
Qy	1261	TCACTTCTCAGACCGGGGATGCGGAGATGGCCATCGCACTCTGGAACCAATGCTGGA	1320
Db	3865	TCACTTCTCAGACCGGGGATGCGGAGATGGCCATCGCACTCTGGAACCAATGCTGGA	3924
Qy	1321	ACAGTGGCGGCAAGACTACCTCCAACTTTCACCCACAGCGGAGCAAACTCAAGTG	1380
Db	3925	ACAGTGGCGGCAAGACTACCTCCAACTTTCACCCACAGCGGAGCAAACTCAAGTG	3984
Qy	1381	CCCTCTCTCAGAGCCCTTACCTCTACACCTTGGGACAGCGGATGCTCCAGACCA	1440
Db	3985	CCCTCTCTCAGAGCCCTTACCTCTACACCTTGGGACAGCGGATGCTCCAGACCA	4044
Qy	1441	GGCTGAAGAGCCCGGAGGTCTACTTGGGCTGTCCAGTGGCGAGGAGTGGGCTT	1500
Db	4045	GGCTGAAGAGCCCGGAGGTCTACTTGGGCTGTCCAGTGGCGAGGAGTGGGCTT	4104
Qy	1501	TGTGTTGGGCAATCATCGGACAGTGTGTGAGGTGACAGAGAGTGGCGGAGGAGA	1560
Db	4105	TGTGTTGGGCAATCATCGGACAGTGTGTGAGGTGACAGAGAGTGGCGGAGGAGA	4164
Qy	1561	TGCTCCATGAGCTTGGCCTCTAGGCGCGGGGTGGGTCTCTCAACCTTAA	1620
Db	4165	TGCTCCATGAGCTTGGCCTCTAGGCGCGGGGTGGGTCTCTCAACCTTAA	4224

RESULT 3

AD018837	ID	AD018837	standard; DNA; 4512 BP.
XX	AC	AD018837;	
XX	DT	12-AUG-2004	(first entry)
XX	DE	Human lipid-associated molecule (LIPAM) gene SeqID32.	
XX	XX	Lipid-associated molecule; LIPAM; neuroprotective; relaxant; antithyroid;	
KW	KW	antidiabetic; cytotatic; dermatological; immunosuppressive;	
KW	KW	antiinflammatory; thyromimetic; antiallergic; cerebroprotective;	
KW	KW	gastrointestinal; hepatotropic; nephrotropic; anticonvulsant;	
KW	KW	antiparkinsonian; antibacterial; antiparasitic; fungicide; protozoacide;	
KW	KW	viricide; uropathic; antirheumatic; cardiant; cardiovascular; anti-HIV;	
KW	KW	neotropic; LIPAM agonist; LIPAM antagonist; gene therapy;	
KW	KW	neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;	
KW	KW	muscular disorder; myotonic dystrophy; cataract; endocrine disorder;	
KW	KW	Grave's disease; cancer; leukaemia; cervical; breast cancers;	
KW	KW	immunological disorder; scleroderma; systemic lupus erythematosus;	
KW	KW	allergy; gastrointestinal disorder; Crohn's disease; renal disorder;	
KW	KW	Goodpasture's syndrome; infection; viral; bacterial; fungal; parasitic;	
KW	KW	protozoal; helminthic; cardiovascular disorder; atherosclerosis;	
KW	KW	hepatic disease; cirrhosis; transgenic animal; gene; ds; human.	
XX	OS	Homo sapiens.	
XX	XX	WO2004044165-A2.	
XX	PN	27-MAY-2004.	
XX	PD		
XX	PF	10-NOV-2003; 2003WO-US035946.	
XX	XX	13-NOV-2002; 2002US-0426105P.	
PR	PR	12-DEC-2002; 2002US-0433215P.	
PR	PR	07-MAR-2003; 2003US-0453127P.	
PR	PR	13-MAR-2003; 2003US-0454801P.	
PR	PR	24-APR-2003; 2003US-0465495P.	
PR	PR	24-APR-2003; 2003US-0465619P.	
PR	PR	01-AUG-2003; 2003US-0491800P.	
XX	XX	(INCY-) INCYTE CORP.	
XX	XX	Jiang X, Becha SD, Bulloch SA, Chang H, Chawla NK, Elliott VS;	
PI	PI	Emerling BM, Gietzen KJ, Hafalia AJA, Jackson AA, Kable AE, Khare R;	
PI	PI	Lee SY, Marquis JP, Muraige J, Swarnakar A, Yang YG;	
XX	XX	WPI; 2004-420307/39.	
DR	DR	P-PSDB; AD018816.	
XX	XX	New LIPAM polypeptides, useful for diagnosing, preventing, and treating	
PT	PT	disorders associated with abnormal expression or activity of LIPAM, e.g.	
PT	PT	neuromuscular, immunological, cardiovascular disorders, cancer and/or	
PT	PT	infections.	

XX Claim 5; SEQ ID NO 32; 207pp; English.
PS This invention relates to novel human lipid-associated molecules (LIPAM)
XX and the DNA sequences which encode them. The invention may be useful for
CC the production of compounds with a neuroprotective, relaxant,
CC antithyroid, antidiabetic, cytostatic, dermatological, immunosuppressive,
CC antiinflammatory, thymimetic, antiallergic, cerebroprotective,
CC gastrointestinal, hepatotropic, nephrotropic, anticonvulsant,
CC antiparkinsonian, antibacterial, antiparasitic, fungicide, protozoacide,
CC virucide, uropathic, antirheumatic, cardiant, cardiovascular, anti-HIV or
CC nootropic activity acting as LIPAM agonists or antagonists. In addition,
CC the disclosed sequences may be useful for gene therapy. The invention may
CC be useful for diagnosing, preventing, and treating disorders associated
CC with an abnormal expression or activity of LIPAM, such as
CC neurodegenerative disorders (for example Parkinson's disease, Alzheimer's
CC disease), muscular disorders (for example myotonic dystrophy, catatonina),
CC endocrine disorders (for example diabetes, Grave's disease), cancers (for
CC example leukemia, cervical or breast cancers), immunological disorders
CC (for example scleroderma, systemic lupus erythematosus, allergies),
CC gastrointestinal disorders (for example Crohn's disease), renal disorders
CC (for example Goodpasture's syndrome), infections (for example viral,
CC bacterial, fungal, parasitic, protozoal, helminthic), cardiovascular
CC disorders (for example atherosclerosis), or hepatic diseases (for example
CC cirrhosis). LIPAM or its fragments may also be used in screening for
CC compounds that specifically bind to and modulate the activity of LIPAM.
CC The polynucleotides can be used to create humanised animals or transgenic
CC animals to model human disease. The present sequence is that of a human
CC lipid-associated molecule (LIPAM) gene of the invention.

XX
SQ Sequence 4512 BP; 1115 A; 1266 C; 1182 G; 949 T; 0 U; 0 Other;

Query Match 88.7%; Score 1627.8; DB 12; Length 4512;
Best Local Similarity 93.6%; Pred. No. 0;
Matches 1778; Conservative 0; Mismatches 2; Indels 119; Gaps 3;

Qy 1 CTGAGCCCACTTTGTTGACCATCTCGCAATGCTTGGAGCTCTGATAGAGAGCTTT 60
Db CTGAGCCCACTTTGTTGACCATCTCGCAATGCTTGGAGCTCTGATAGAGAGCTTT 60
Qy 61 TCCCTTAGTGTCCAGAGTCTGTGTCACCTCGTGAGCTTCTGAACCCCACTATATGC 120
Db AGGTGCCAGAGTCTGTGTCACCTCGTGAGCTTCTGAACCCCACTATATGC 2733
Qy 121 GGCAGGTGTTCTTGGGAAACCCAGACAGTGTCCAGTGCAGAGCCAGAGCAGATGCG 180
Db GGCAGGTGTTCTTGGGAAACCCAGACAGTGTCCAGTGCAGAGCCAGAGCAGATGCG 2793
Qy 181 CGAGCTGTGGGTTCAGGCGCTATGACAGCAGAGAGATTTCTGTGTGTGTGAGCC 240
Db CGAGCTGTGGGTTCAGGCGCTATGACAGCAGAGAGATTTCTGTGTGTGTGAGCC 2853
Qy 241 CTCTTCCAGAACATCCAGCTCCCTGTCTGCGC----- 273
Db CTCTTCCAGAACATCCAGCTCCCTGTCTGCGC----- 2913
Qy 274 ----- 273
Db TGCCCCAGATGTCATCCACCAATCAGAAATTCATCCAGCTGGCCAGAGCCCTTTG 2973
Qy 274 -----GTTGAAACACTTGGAGCAAAACAGAGACCTTGACCTTGAGAGAGAT 324
Db GACCAATATGTTGAAACCACTTGGAGCAAAACAGAGACCTTGACCTTGAGAGAGAT 3033
Qy 325 GCCCATCCTGTCCCACTCAGATGAGCCCTTCTGAGAACCCCTCGGAATAGTAATA 384
Db GCCCATCCTGTCCCACTCAGATGAGCCCTTCTGAGAACCCCTCGGAATAGTAATA 3093
Qy 385 CAGCTACCCCATCAAGCCAGCCCAATTGAAACTGGGCGAGTGACTTCTGTGTACAGAGTG 444
Db CAGCTACCCCATCAAGCCAGCCCAATTGAAACTGGGCGAGTGACTTCTGTGTACAGAGTG 3153
Qy 3094 CAGCTACCCCATCAAGCCAGCCCAATTGAAACTGGGCGAGTGACTTCTGTGTACAGAGTG 3153
Qy 445 GAAGGCTTCCAAATAGTGTTCAAACCTCTGTGTCCACCAAGCTCCGACGACGACATCAAAAGT 504

Db 3154 GAAGGCTTCCAAATAGTGTTCAAACCTCTGTGTCCACAGCTCCGACAGACATCAAAAGT 3213
Qy 505 GGTGCGCGCCCTCGGTGTGACTCTCTGACTACAGCAGTGGAGCTCCACAAACAACTCCAG 564
Db 3214 GGTGCGCGCCCTCGGTGTGACTCTCTGACTACAGCAGTGGAGCTCCACAAACAACTCCAG 3273
Qy 565 TGACCTACCCACATCTTTGGAGGGGACTCTCTTTGGAGCAATTTGGAGGGGATGGAACTTGA 624
Db 3274 TGACCTACCCACATCTTTGGAGGGGACTCTCTTTGGAGCAATTTGGAGGGGATGGAACTTGA 3333
Qy 625 GACTCACACACACTGCCCAACATTTGAGAGAGTTCAACCTTTACCTCTCTTGGTCTTC 684
Db 3334 GACTCACACACACTGCCCAACATTTGAGAGAGTTCAACCTTTACCTCTCTTGGTCTTC 3393
Qy 685 TACCAGACCTTGGAGGGGACAGCAGGACTAAATGTGACGCGGAGGGCCAGAGCTAG 744
Db 3394 TACCAGACCTTGGAGGGGACAGCAGGACTAAATGTGACGCGGAGGGCCAGAGCTAG 3453
Qy 745 GGACATGCCAGCCCGAGGCTGGGACCTTGGTAGAGCGAATGAAACACGCCCCGACATCAA 804
Db 3454 GGACATGCCAGCCCGAGGCTGGGACCTTGGTAGAGCGAATGAAACACGCCCCGACATCAA 3513
Qy 805 CTTGAGAGAGACTGGAGCTGTGTCACACTCTTCAATTTGGGGTCAACGACTTGTGTCTA 864
Db 3514 CTTGAGAGAGACTGGAGCTGTGTCACACTCTTCAATTTGGGGTCAACGACTTGTGTCTA 3573
Qy 865 CTGTGAGAACTCCGAGGCGCCACTTTGGCCACCGAATATGTTTCCAGCAGATCCCAACGAGCCCT 924
Db 3574 CTGTGAGAACTCCGAGGCGCCACTTTGGCCACCGAATATGTTTCCAGCAGATCCCAACGAGCCCT 3633
Qy 925 GGAATCTCTCTCTGAGGAGCTCCCAAGGGCTTTTCTCAACCTGTGTGGAGGTCAATGAGCT 984
Db 3634 GGAATCTCTCTCTGAGGAGCTCCCAAGGGCTTTTCTCAACCTGTGTGGAGGTCAATGAGCT 3693
Qy 985 GGCTAGCTGTGTCAGGGCCAGGCGGGAATGTGCCATGTCTGGCAGCTCAGAACCACTG 1044
Db 3694 GGCTAGCTGTGTCAGGGCCAGGCGGGAATGTGCCATGTCTGGCAGCTCAGAACCACTG 3753
Qy 1045 CACTTGTCTCAGACACTCGCAAGCTCCCTGGAGAACCAAGAACTGGAAGAGTGAACCTG 1104
Db 3754 CACTTGTCTCAGACACTCGCAAGCTCCCTGGAGAACCAAGAACTGGAAGAGTGAACCTG 3813
Qy 1105 GAACCTCCAGCATGGCATCTCCAGTTTCTCTCTGACCAATAACAACAGCTGAGGAG 1164
Db 3814 GAACCTCCAGCATGGCATCTCCAGTTTCTCTCTGACCAATAACAACAGCTGAGGAG 3873
Qy 1165 CTTTGGGTTGTGTGAGGCTTTCTTCCAAAAACAACCTCAACCTCAACCTCAACCTCAACCT 1217
Db 3874 CTTTGGGTTGTGTGAGGCTTTCTTCCAAAAACAACCTCAACCTCAACCTCAACCTCAACCT 3933
Qy 1218 ----AGAGAGGGGACACTGACCTCAGCTTCTTCCAGGAGCTGTTTCACTTCTCAGAC 1273
Db 3934 CTGACAGAGAGGGGACACTGACCTCAGCTTCTTCCAGGAGCTGTTTCACTTCTCAGAC 3993
Qy 1274 CGCGGGATGCCAGATGGCCATCGCACTCTGGAACCAACATGCTGGAACCAACATGCTGGCCGC 1333
Db 3994 CGCGGGATGCCAGATGGCCATCGCACTCTGGAACCAACATGCTGGAACCAACATGCTGGCCGC 4053
Qy 1334 AAGACTACCTCCAAACAACTTCAACCAAGCGAGCCAAACCTCAAGTGCCCTCTCTCTGAG 1393
Db 4054 AAGACTACCTCCAAACAACTTCAACCAAGCGAGCCAAACCTCAAGTGCCCTCTCTCTGAG 4113
Qy 1394 AGCCCTTACCTTACACCTTGGGAAACAGCGGATGCTCCAGACAGGCTGGAAGAGCC 1453
Db 4114 AGCCCTTACCTTACACCTTGGGAAACAGCGGATGCTCCAGACAGGCTGGAAGAGCC 4173
Qy 1454 CCGAGGTGTCTACTGGGCTGTCCAGTGGCGGAGTGGGCTTGTGGTGGGATC 1513
Db 4174 CCGAGGTGTCTACTGGGCTGTCCAGTGGCGGAGTGGGCTTGTGGTGGGATC 4233
Qy 1514 ATCGGGAACATGTGTCTGGAGGTGACGAGAGGTGGCGGAGGAGATCTCTCCAAATGAGC 1573

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Db 4234 ATCGGACAGTGGTCTGGAGGTGCAGAGAGAGTGGCCGGAGGAGATCTCCATGAGC 4293

Qy 1574 CTGCGCACTGTGGCCCTCTAGGCGCGGGGGTCTTCACCCCTAACTCCCTATAGCCA 1633

Db 4294 CTGCGCACTGTGGCCCTCTAGGCGCGGGGGTCTTCACCCCTAACTCCCTATAGCCA 4353

Qy 1634 CTCTCTTACCGCCCTCTGCGCCAGCCACTCCCGCCACAGGACATGCTTCAATGCTG 1693

Db 4354 CTCTCTTACCGCCCTCTGCGCCAGCCACTCCCGCCACAGGACATGCTTCAATGCTG 4413

Qy 1694 GTCCCATAGAGAGCCAGGAGGACAGTCAACAATCTTCTGGGGCTGGGCTTCTTCAGGCC 1753

Db 4414 GTCCCATAGAGAGCCAGGAGGACAGTCAACAATCTTCTGGGGCTGGGCTTCTTCAGGCC 4473

Qy 1754 TATGCTCTCGAATGATACATTTAATAAAGTCCAAAG 1792

Db 4474 TATGCTCTCGAATGATACATTTAATAAAGTCCAAAG 4512

RESULT 4

AAD52626

ID AAD52626 standard; cdna; 4607 BP.

XX AAD52626;

AC AAD52626;

XX 14-MAY-2003 (first entry)

XX Human lipid-associated molecule (LIPAM)-1 cDNA.

DE Human; lipid-associated molecule; LIPAM; cardiovascular disorder; stroke;

XX Human; arteriovenous fistula; atherosclerosis; hypertension; Raynaud's disease;

XX aneurysm; congestive heart failure; thrombophlebitis; angina pectoris;

KW ischaemic heart disease; rheumatic heart disease; peptic oesophagitis;

KW gastrointestinal disorder; lipid metabolism disorder; Crohn's disease;

KW nausea; peptic ulcer; fatty liver; Fabry's disease; Gaucher's disease;

KW diabetes mellitus; hyperlipidaemia; hypercholesterolaemia; epilepsy;

KW autoimmune disorder; inflammatory disorder; neurological disorder; kuru;

KW acquired immunodeficiency syndrome; anaemia; Alzheimer's disease; asthma;

KW dementia; prion disease; Creutzfeldt-Jakob disease; leukaemia; cancer;

KW adenocarcinoma; lymphoma; melanoma; myeloma; sarcoma; gene therapy;

KW protein replacement therapy; gene; ss.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX 9..4385

XX /tag= a

XX /product= "Human LIPAM-1 protein"

XX CDS

XX 9..89

XX /tag= j

XX sig_peptide

XX 9..77

XX /tag= h

XX sig_peptide

XX 9..74

XX /tag= f

XX sig_peptide

XX 9..71

XX /tag= d

XX sig_peptide

XX 9..65

XX /tag= b

XX mat_peptide

XX 66..4382

XX /tag= c

XX /product= "Human mature LIPAM-1 protein"

XX 72..4382

XX /tag= e

XX mat_peptide

XX 75..4382

XX /product= "Human mature LIPAM-1 protein"

XX mat_peptide

XX 78..4382

XX /tag= g

XX /product= "Human mature LIPAM-1 protein"

XX mat_peptide

XX 80..4382

XX /tag= i

XX /product= "Human mature LIPAM-1 protein"

XX mat_peptide

XX 90..4382

XX /tag= k

XX /product= "Human mature LIPAM-1 protein"

XX mat_peptide

XX WO200294988-A2.

XX 28-NOV-2002.

XX 17-MAY-2002; 2002WO-US015688.

XX 18-MAY-2001; 2001US-0292242P.

XX 25-MAY-2001; 2001US-0293726P.

XX 01-JUN-2001; 2001US-0293346P.

XX 06-JUL-2001; 2001US-0303404P.

XX 24-AUG-2001; 2001US-0314754P.

XX 22-JAN-2002; 2002US-0351262P.

XX 29-MAR-2002; 2002US-0368799P.

XX (INCY-) INCYTE GENOMICS INC.

XX Tang YT, Yue H, Azimzai Y, Baughn MR, Burford N, Reddy R;

XX Walia NK, Das D, Nguyen DB, Yao MG, Arvizu CS, Lu Y, Gandhi AR;

XX Griffin JA, Elliott VS, Ramkumar J, Lal PG, Lu DAM, Lee EA, Lee SY;

XX Yue H, Yang J, Tribouley CW, Kable AE, Swarnakar A;

XX WPI; 2003-120797/11.

XX P-PSDB; AAE34440.

XX New human lipid-associated molecule (LIPAM) proteins and polynucleotides,

XX useful for diagnosing, treating or preventing cardiovascular disorders

XX (e.g. aneurysms), neurological disorders (e.g. Parkinson's disease) or

XX cancers.

XX Claim 66; Page 158-159; 171pp; English.

XX The present invention relates to novel human lipid-associated molecules

XX (LIPAM) and polynucleotides encoding such proteins. Sequences of the

XX invention are useful for treating diseases or conditions associated with

XX decreased expression of functional LIPAM. The antagonist is useful for

XX treating a disease or condition associated with the overexpression of

XX functional LIPAM. They are useful for diagnosing, treating or preventing

XX cardiovascular disorders (e.g. arteriovenous fistula, atherosclerosis,

XX hypertension, Raynaud's disease, angina pectoris, varicose veins, congestive

XX heart failure, thrombophlebitis, gastrointestinal disorders (e.g. peptic

XX or rheumatic heart disease), gastric ulcer or Crohn's disease), lipid metabolism

XX disorders (e.g. fatty liver, Fabry's disease, Gaucher's disease, diabetes

XX mellitus, hyperlipidaemia, hypercholesterolaemia), autoimmune disorders

XX or inflammatory disorders (e.g. acquired immunodeficiency syndrome,

XX anaemia, asthma or Crohn's disease), neurological disorders (e.g. stroke,

XX epilepsy, dementia, Alzheimer's disease, or prion diseases such as kuru

XX or Creutzfeldt-Jakob disease) or cancers (e.g. adenocarcinoma, leukaemia,

XX lymphoma, melanoma, myeloma or sarcoma). They are also used in gene

XX therapy and protein replacement therapy. The present sequence is human

XX LIPAM-1 cDNA

XX SQ

Query Match 84.8%; Score 1555.2; DB 8; Length 4607;

Best Local Similarity 90.2%; Pred. No. 0;

Matches 1799; Conservative 0; Mismatches 3; Indels 192; Gaps 5;

Qy 1 CTGCGCCAACTTTGTTGACCATCTCCGCAATGCTTGGACCTCTCGATAGAGAGCTTT 60

Db 2626 CTGCGCCAACTTTGTTGACCATCTCCGCAATGCTTGGACCTCTCGATAGAGAGCTTT 2679

Qy 61 TCCCTTAGGTGCCAGAGTCTCGTCACTCGTGGACTTCTTGAACCCCACTATCATGC 120

Db 2680 -----AGGTGCCAGAGTCTCGTCACTCGTGGACTTCTTGAACCCCACTATCATGC 2733

Qy 121 GGCAGGTGTTCTCTGGGAAACCCAGACAAAGTCCAGTGCAGCAGGCGAGTGTGTA 168

Db 2734 GGCAGGTGTTCTCTGGGAAACCCAGACAAAGTCCAGTGCAGCAGGCGAGTGTGTA 2793

Qy 169 ----- 168

Db 2794 ACTGGTTCTGACCCCTGCGGGAGAACTCCCAAGAGCTAGCCAGGCTGAGGCGCTTCAGCC 2853
Qy 169 -----GAGCAGCATGCGGAGCTGGTGGGTGAGGCGGCTATGACACGAGGAGG 218
Db 2854 GAGCCTACCGGAGCAGCATGCGGAGCTGGTGGGTGAGGCGGCTATGACACGAGGAGG 2913
Qy 219 ACTTCTCTGTGTGTGAGGCGCTTCCTCCAGAACTCCAGCTCCCTGTCTGTGCG- 273
Db 2914 ACTTCTCTGTGTGTGAGGCGCTTCCTCCAGAACTCCAGCTCCCTGTCTGTGCGGATG 2973
Qy 274 ----- 273
Db 2974 GGCTCCCGATACGTCCTCTTTGTCGCCAGACTGATCCACCCAAATCAGAAATTCACACT 3033
Qy 274 -----GCTTGAACCACTTGGAGCAAAACAGAGA 302
Db 3034 CCCAGCTGGCCAGAGCCCTTTGGACCAATATGCTTGAACCACTTGGAGCAAAACAGAGA 3093
Qy 303 CCCTGGACCTGAGAGCAGAGATGGCGATCACTGTCCCACTCAGAAATGAGGCCCTTCCTGA 362
Db 3094 CCCTGGACCTGAGAGCAGAGATGGCGATCACTGTCCCACTCAGAAATGAGGCCCTTCCTGA 3153
Qy 363 GAACCCCTCGGAATAGTAACCTACAGCTACCCCATCAAGCCAGCCATTGAGAACTGGGGCA 422
Db 3154 GAACCCCTCGGAATAGTAACCTACAGCTACCCCATCAAGCCAGCCATTGAGAACTGGGGCA 3213
Qy 423 GTGACTTCTGTGTACAGAGTGGAGGCTTCCAAATAGTGTTCCAACCTCTGTCCACCAGC 482
Db 3214 GTGACTTCTGTGTACAGAGTGGAGGCTTCCAAATAGTGTTCCAACCTCTGTCCACCAGC 3273
Qy 483 TCCAGCAGCAGACATCAAAAGTGTGGCGGCCCTTGGGTGACTCTCTGACTACAGAGTGG 542
Db 3274 TCCAGCAGCAGACATCAAAAGTGTGGCGGCCCTTGGGTGACTCTCTGACTACAGAGTGG 3333
Qy 543 GAGCTCGACCAAAACAACTCCAGTCACTTACCCACATCTTGGAGGGGACTCTCTTGGAGCA 602
Db 3334 GAGCTCGACCAAAACAACTCCAGTCACTTACCCACATCTTGGAGGGGACTCTCTTGGAGCA 3393
Qy 603 TTGAGGGGATGGAACTTTGAGAGCTCACACACACTGCCCAACATCTGAAAGATTCA 662
Db 3394 TTGAGGGGATGGAACTTTGAGAGCTCACACACACTGCCCAACATCTGAAAGATTCA 3453
Qy 663 ACCCTTACCTCTTGGCTTCTACAGAGCTCGGGAGGGGACAGAGGACTAAATGTGG 722
Db 3454 ACCCTTACCTCTTGGCTTCTACAGAGCTCGGGAGGGGACAGAGGACTAAATGTGG 3513
Qy 723 CAGCGAAGGGCCAGAGCTAGGACATGCCAGCCAGGCTGGGACTGTAGAGCGAA 782
Db 3514 CAGCGAAGGGCCAGAGCTAGGACATGCCAGCCAGGCTGGGACTGTAGAGCGAA 3573
Qy 783 TGA AAAA CAGCCCGACATCAACCTGGAGAAAGACTGGAAGCTGGTCACTCTTCATTG 842
Db 3574 TGA AAAA CAGCCCGACATCAACCTGGAGAAAGACTGGAAGCTGGTCACTCTTCATTG 3633
Qy 843 GGGTCAACGACTTGTGTCTTACTGAGAGATCCGAGGGCCCACTTGGCCACGGAATATG 902
Db 3634 GGGTCAACGACTTGTGTCTTACTGAGAGATCCGAGGGCCCACTTGGCCACGGAATATG 3693
Qy 903 TTCAAGCAGATCCAAAGCCCTGGACATCTCTCTGAGGAGCTCCAGGGCTTTCCTCA 962
Db 3694 TTCAAGCAGATCCAAAGCCCTGGACATCTCTCTGAGGAGCTCCAGGGCTTTCCTCA 3753
Qy 963 ACCTGGTGGAGGTCTATGGAGCTGAGCTAGCTGTACCAAGGGCCAAAGGGGAAATGTGCCA 1022
Db 3754 ACCTGGTGGAGGTCTATGGAGCTGAGCTAGCTGTACCAAGGGCCAAAGGGGAAATGTGCCA 3813
Qy 1023 TGCTGGCAGCTCAGAAACAACTGCACTTGTGCTCAGACACTGCGAAAGCTCCCTGGAGAGC 1082
Db 3814 TGCTGGCAGCTCAGAAACAACTGCACTTGTGCTCAGACACTGCGAAAGCTCCCTGGAGAGC 3873
Qy 1083 AAGAACTGAAAGATGAACTGGAACTCCAGCATGCGATCTCCAGTTCTCTCTACTGGC 1142
Db 3874 AAGAACTGAAAGATGAACTGGAACTCCAGCATGCGATCTCCAGTTCTCTCTACTGGC 3933

Qy 1143 ACCAATACACACAGCGTGAGGACTTTGCGGTGTGGTGACGCTTTCTTCCAAACACAC 1202
Db 3934 ACCAATACACACAGCGTGAGGACTTTGCGGTGTGGTGACGCTTTCTTCCAAACACAC 3993
Qy 1203 TCACCCCACTGAACGAGAGAGGGGACACTGACCTCACTTCTTCCGAGGACTGTGTTTC 1262
Db 3994 TCACCCCACTGAACGAGAGAGGGGACACTGACCTCACTTCTTCCGAGGACTGTGTTTC 4053
Qy 1263 ACTTCTCAGACCGGGGATGCGAGATGGCCATCGCACTCTGGAACAACATGCTGGAAC 1322
Db 4054 ACTTCTCAGACCGGGGATGCGAGATGGCCATCGCACTCTGGAACAACATGCTGGAAC 4113
Qy 1323 CAGTGGCCCGCAAGACTACCTTCCAAACAACTTCAACCCAGCCGAGCCAAAATCAAGTGCC 1382
Db 4114 CAGTGGCCCGCAAGACTACCTTCCAAACAACTTCAACCCAGCCGAGCCAAAATCAAGTGCC 4173
Qy 1383 CCTCTCTGAGAGCCCTTACCTCTACACCTTGGCGAAACAGCGATTTGTCACAGACGAG 1442
Db 4174 CCTCTCTGAGAGCCCTTACCTCTACACCTTGGCGAAACAGCGATTTGTCACAGACGAG 4233
Qy 1443 CTGAAGAAGCCCGGAGGTGCTCTACTGGGTGTCCCAAGTGGCAGCGGAGTCCGCTTG 1502
Db 4234 CTGAAGAAGCCCGGAGGTGCTCTACTGGGTGTCCCAAGTGGCAGCGGAGTCCGCTTG 4293
Qy 1503 TGGTGGGCATCATCGGACAGTGGTCTGAGAGTGCAGGAGAGTGGCCGGAGGGAAGATC 1562
Db 4294 TGGTGGGCATCATCGGACAGTGGTCTGAGAGTGCAGGAGAGTGGCCGGAGGGAAGATC 4353
Qy 1563 CTCAATAGAGCTGGGCACTGTGGCCCTCTAGGCCCGGGGGTGGGTCTCAACCTAAACT 1622
Db 4354 CTCAATAGAGCTGGGCACTGTGGCCCTCTAGGCCCGGGGGTGGGTCTCAACCTAAACT 4413
Qy 1623 CCTATAGCCACTCTCTTACCGCCCTGCCCCAGCCACTCCCGGCCACCCAGGACATGC 1682
Db 4414 CCTATAGCCACTCTCTTACCGCCCTGCCCCAGCCACTCCCGGCCACCCAGGACATGC 4473
Qy 1683 TTC-AATGCTGTGTGCCATAGGAAGCCCA-GGGGACAGTCACTTCTTGGGGCTTGGG 1740
Db 4474 TTC-AATGCTGTGTGCCATAGGAAGCCCA-GGGGACAGTCACTTCTTGGGGCTTGGG 4533
Qy 1741 CTTCTTCCAGGCTATGCTCTCTGGAATGGATATCAATTTAAATAAAGTCAAAAGCTATTTTA 1800
Db 4534 CTTCTTCCAGGCTATGCTCTCTGGAATGGAAACATTTAAATAAAGTCAAAAGCTATTTTA 4593
Qy 1801 AAAAAAAAAAAAAA 1814
Db 4594 AAAAAAAAAAAAAA 4607

RESULT 5

ADH13733

ID ADH13733 standard; DNA; 4311 BP.

XX AC ADH13733;

XX AC ADH13733;

DT 11-MAR-2004 (first entry)

XX AC ADH13733;

XX AC ADH13733;

XX AC ADH13733;

XX AC ADH13733;

human; ENZM; cytostatic; antiarteriosclerotic; anticonvulsant; nootropic;
neuroprotective; cerebroprotective; anti-HIV; anti-allergic;
anti-inflammatory; thymoprotective; gene therapy;
cell proliferative disorder; cancer; atherosclerosis;
neurological disorder; epilepsy; Huntington's disease; stroke;
immune disorder; inflammatory disorder; AIDS; allergy;
developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
gene; db.

OS Homo sapiens.

XX AC ADH13733;

XX AC ADH13733;

XX AC ADH13733;

XX AC ADH13733;

us-09-778-961-1.rng

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13-NOV-2003.
 29-APR-2003; 2003WO-US013821.
 29-APR-2002; 2002US-0376506P.
 17-MAY-2002; 2002US-0381558P.
 (INCY-) INCYTE CORP.
 Khare R, Kable AE, Lee SY, Hafalia AJA, Chawla NK, Marquis JP;
 Ramkumar J, Wilson AD, Jin P, Hawkins PR, Bulloch SA, Swarnakar A;
 Elliott VS, Richardson TW, Mason PM, Baughn MR, Yue H, Becha SD;
 Tang YT, Batra S, Lu DAM, Bhatia UG, Burrill JD, Lee S, Blake JU;
 Ho A, Zheng W, Gao J;
 WPI: 2004-053042/05.
 P-PSDB; ADH13664.
 New human enzymes (ENZM), useful for diagnosing, treating and preventing
 diseases or conditions associated with the aberrant ENZM expression e.g.
 cancer, AIDS, atherosclerosis, epilepsy, or infections.
 Claim 5; SEQ ID NO 86; 463pp; English.
 This invention relates to novel human enzymes (ENZM) and the genes which
 encode them. The invention may be useful for the development of compounds
 with a cytostatic, antiarteriosclerotic, anticonvulsant, nootropic,
 neuroprotective, cerebroprotective, anti-HIV, antiallergic,
 antiinflammatory or thymometric activity or for gene therapy. The
 invention may therefore be useful in diagnosing, treating and preventing
 diseases or conditions associated with the decreased expression or
 overexpression of ENZM, such as cell proliferative (for example cancer,
 atherosclerosis), neurological (for example epilepsy, Huntington's
 disease, stroke), immune/inflammatory (for example AIDS, allergies) and
 developmental (for example Hypothyroidism, Cushing's syndrome) disorders
 or infections. These are also useful in assessing the effects of
 exogenous compounds on the expression of nucleic acid and amino acid
 sequences of ENZM. The present sequence is that of a gene which encodes a
 human ENZM enzyme of the invention.
 Sequence 4311 BP; 1076 A; 1130 C; 907 T; 0 U; 0 Other;
 Query Match 82.5%; Score 1513.8; DB 12; Length 4311;
 Best Local Similarity 92.8%; Pred. No. 0;
 Matches 1673; Conservative 0; Mismatches 2; Indels 128; Gaps 3;
 1 CTGACGCAACTTTGTTGACCATCTCCGCAATGCCCTTGGACGCTCTGATAGAGCTTT 60
 2626 CTGACGCAACTTTGTTGACCATCTCCGCAATGCCCTTGGACGCTCTGATAGAG 2679
 61 TCCCTTAGGTGCCCAGAGTCTGGTCAACTCGTGACTTCTGTAACCCCACTATATGC 120
 2680 -----AGGTGCCAGAGTCTGGTCAACTCGTGACTTCTGTAACCCCACTATATGC 2733
 121 GGCAGGTGTTCTGGGAAACCCAGACAGTGCCTGAGTGCAGGAGCCAGAGCATGCG 180
 2734 GGCAGGTGTTCTGGGAAACCCAGACAGTGCCTGAGTGCAGGAGCCCA ----- 2781
 181 CGAGCTGGTGGGTGAGCGCCGCTATGACGCGAGGAGGACTTCTGTGTGCTGCAGCC 240
 2782 ----- 2781
 241 CTTCTTCAGNACATCCAGCTCCCTGCTGGCGCTTGAACCACTTGGAGCAAAACAGA 300
 2782 -----GCTTGAACCACTTGGAGCAAAACAGA 2808
 301 GACCTTGACCTGAGAGCAGAGATGCCCATCACTGTGCCACTCAGANTGAGCCCTTCT 360
 2809 GACCTTGACCTGAGAGCAGAGATGCCCATCACTGTGCCACTCAGANTGAGCCCTTCT 2868
 361 GAGAACCCCTCGGATAGTACTACCTACCTACCCATCAAGCCAGCCATTGAGAACTGGG 420
 2869 GAGAACCCCTCGGATAGTACTACCTACCTACCCATCAAGCCAGCCATTGAGAACTGGG 2928

QY 421 CAGTCACTTCTGTGTATACAGAGTGAAGGCTTCAATAGTCTTCAACCTCTGTCCACCA 480
 DB 2929 CAGTCACTTCTGTGTATACAGAGTGAAGGCTTCAATAGTCTTCAACCTCTGTCCACCA 2988
 QY 481 GCTCCGACAGCAGACATCAAAAGTGTGGCGCGCTTGGTGAAGTCTCTGTGACTACAGAGT 540
 DB 2989 GCTCCGACAGCAGACATCAAAAGTGTGGCGCGCTTGGTGAAGTCTCTGTGACTACAGAGT 3048
 QY 541 GGGAGCTCGACCAAACTCCAGTGAAGTCTTGGAGGGGAGTCTCTTGGAG 600
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 QY 601 CATTTGAGGGGATGGAACTTTGGAGACTCACACCACTGCCCCAATCTTGAAGAAGTT 660
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 QY 661 CAACCCCTTACCTCTTGGCTTCTTACAGACCTTGGAGGGGAGTCTTAAATGT 720
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 QY 721 GGCAGCGGAAGGGGCGAGAGTGGAGCATGCGAGCCAGGCTTGGAGCTTGGTGAAGCG 780
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 QY 781 AATCAAAAACAGCCCCGACATCAACCTGGAGAAAGTCTGGAAGTCTGTCACACTTTCAT 840
 DB 3289 AATCAAAAACAGCCCCGACATCAACCTGGAGAAAGTCTGGAAGTCTGTCACACTTTCAT 3348
 QY 841 TGGGGTCAACGACTTGTCTTACTTGTGAGAAATCCGAGGGCCCTTGGCCACCGAATA 900
 DB 3349 TGGGGTCAACGACTTGTCTTACTTGTGAGAAATCCGAGGGCCCTTGGCCACCGAATA 3408
 QY 901 TGTTCAGACATCAACAGGCGCTTGGACATCTCTCTGTGAGAGTCTCCAGAGGCTTTCGT 960
 DB 3409 TGTTCAGACATCAACAGGCGCTTGGACATCTCTCTGTGAGAGTCTCCAGAGGCTTTCGT 3468
 QY 961 CAACTGTGTGAGGTCTGAGCTGAGTGTGCTGTACAGGGCCAGGGCGGAAATGTC 1020
 DB 3469 CAACTGTGTGAGGTCTGAGCTGAGTGTGCTGTACAGGGCCAGGGCGGAAATGTC 3528
 QY 1021 CATGTGCGAGCTCAGAAACAACTGCATCTGCTCAGACATCTGCAAAAGTCTCCCTGGAGAA 1080
 DB 3529 CATGTGCGAGCTCAGAAACAACTGCATCTGCTCAGACATCTGCAAAAGTCTCCCTGGAGAA 3588
 QY 1081 GCAAGAACTGAAAGAAAGTGAAGTGAAGTCCAGCATGCTCCAGTCTTCTCTACTG 1140
 DB 3589 GCAAGAACTGAAAGAAAGTGAAGTGAAGTCCAGCATGCTCCAGTCTTCTCTACTG 3648
 QY 1141 GCACCAATACACAGCGGTGAGGACTTTTGGCGTGTGTGCGAGCTTCTTCCAAAACAC 1200
 DB 3649 GCACCAATACACAGCGGTGAGGACTTTTGGCGTGTGTGCGAGCTTCTTCCAAAACAC 3708
 QY 1201 ACTCACCCCACTGAAGCG-----AGAGAGGGGACACTGACTCACCTTCTTCTCC 1249
 DB 3709 ACTCACCCCACTGAAGCGGTGAGTGCAGAGAGGGGACACTGACTCACCTTCTTCTCC 3768
 QY 1250 GAGGACTGTTTCTCACTTCTCAGACCCGCGGCGATGCCAGATGCCATGCGACTCTGGAAC 1309
 DB 3769 GAGGACTGTTTCTCACTTCTCAGACCCGCGGCGATGCCAGATGCCATGCGACTCTGGAAC 3828
 QY 1310 AACATGCTGAAACAGTGGGCGCAAGACTACTTCCAACTTCACTCCACAGCCGAGCC 1369
 DB 3829 AACATGCTGAAACAGTGGGCGCGCAAGACTACTTCCAACTTCACTCCACAGCCGAGCC 3888
 QY 1370 AAACCTGAAGTGGCCCTCTCTGAGAGGCTTACTCTTACACCTCGGGAACAGCCGATG 1429
 DB 3889 AAACCTGAAGTGGCCCTCTCTGAGAGGCTTACTCTTACACCTCGGGAACAGCCGATG 3948
 QY 1430 CTCCAGACCAAGGCTGAAGAAGCCCGAGGCTGTCTACTGGGCTGTCCAGTGGCAGCG 1489
 DB 3949 CTCCAGACCAAGGCTGAAGAAGCCCGCGAGTGTCTACTTGGGCTGTCCAGTGGCAGCG 4008

SQ	Sequence	4425 BP; 1083 A; 1238 C; 1180 G; 924 T; 0 U; 0 Other;
Query Match	77.4%; Score 1421; DB 12; Length 4425;	
Best Local Similarity	88.6%; Pred. No. 0;	
Matches 1695; Conservative	0; Mismatches 10; Indels 208; Gaps 6;	
QY	1 CTGACGCCAATTTTGTGACCAATCTCGCAATGCTTGGAGCTCTGATAGAGCTTT 60	
DB	2540 CTGACGCCAATTTTGTGACCAATCTCGCAATGCTTGGAGCTCTGATAGAG----- 2593	
QY	61 TCCCTTAGTGGCCAGAGTCTGCTCACTCTGCTGAGACTTCTGAAACCCCACTATCATGC 120	
DB	2594 -----AGTGGCCAGAGTCTGCTCACTCTGCTGAGACTTCTGAAACCCCACTATCATGC 2647	
QY	121 GGCAGGTGTTTCTGCGGAACCCAGACAAAGTGCCTCAGTGCAGAGG----- 165	
DB	2648 GGCAGGTGTTTCTGCGGAACCCAGACAAAGTGCCTCAGTGCAGAGG----- 2707	
QY	166 ----- 165	
DB	2708 ACTGCTTCTGACCTCGGGAGAACTCCCAAGAGTAGCCAGCTGGAGGCTTTCAGCC 2767	
QY	166 -----CCAGAGCAGCATGCGGAGCTGGTGGGGTGAAGCCCTATGACAGCAGGAGG 218	
DB	2768 GAGCTTACCAGAGCAGCATGCGGAGCTGGTGGGGTGAAGCCCTATGACAGCAGGAGG 2827	
QY	219 ACTTCTCTGCTGCTGAGCCCTTCTTCCAGAACATCCAGCTCCCTGCTCTG----- 271	
DB	2828 ACTTCTCTGCTGCTGAGCCCTTCTTCCAGAACATCCAGCTCCCTGCTCTGCTGAGGATG 2887	
QY	272 ----- 271	
DB	2888 GGCTCCAGATACGTCCTTCTTGGCCGAGACTGCATCCACCCAAATCAGAAATTCOAAT 2947	
QY	272 -----GGCTTGAACCACTTGGAGCAAAACAGAGA 302	
DB	2948 CCAGCTGGCCAGAGCCCTTTGGACCAATATGCTTGAACCACTTGGAGCAAAACAGAGA 3007	
QY	303 CCCTGGACCTGAGAGCAGAGATGCCATCACTGTCCCACTTCAAGTGAAGCCCTTCTGA 362	
DB	3008 CCCTGGACCTGAGAGCAGAGATGCCATCACTGTCCCACTTCAAGTGAAGCCCTTCTGA 3067	
QY	363 GAAACCCCTCGAATAGTAACTACAGTACCCCATCAAGCCAGCCATTGAGAACTGGGGCA 422	
DB	3068 GAAACCCCTCGAATAGTAACTACAGTACCCCATCAAGCCAGCCATTGAGAACTGGGGCA 3127	
QY	423 GTGACTTCTGTGTGACAGAGTGAAGGCTTCCAAATAGTGTCCAACTCTGTCCACCAAGC 482	
DB	3128 GTGACTTCTGTGTGACAGAGTGAAGGCTTCCAAATAGTGTCCAACTCTGTCCACCAAGC 3187	
QY	483 TCCGACCCAGCAGACATCAAGTGGTGGCCCTGGGTGACTCTCTGACTACAGCAGTGG 542	
DB	3188 TCCGACCCAGCAGACATCAAGTGGTGGCCCTGGGTGACTCTCTGACTACAGCAGTGG 3247	
QY	543 GAGCTCACCAACCACTCCAGTGACTACCCACATCTTGGAGGGGACTCTCTTGGAGCA 602	
DB	3248 GAGCTCACCAACCACTCCAGTGACTACCCACATCTTGGAGGGGACTCTCTTGGAGCA 3307	
QY	603 TTGAGGGGATGGGAATTTGAGACTCACACCACTGCCCACTTCTGAAGAGTTCA 662	
DB	3308 TTGAGGGGATGGGAATTTGAGACTCACACCACTGCCCACTTCTGAAGAGTTCA 3367	
QY	663 ACCCTTACCTCTTGGCTTCTCTACAGACCTTGGAGGGGACAGCAGGACTAAATGTGG 722	
DB	3368 ACCCTTACCTCTTGGCTTCTCTACAGACCTTGGAGGGGACAGCAGGACTAAATGTGG 3427	
QY	723 CAGCGGAAGGGCCAGAGCTAGGAGCATGCCAGCCAGGCTGGACCTGGTAGAGCGAA 782	
DB	3428 CAGCGGAAGGGCCAGAGCTAGGAGCATGCCAGCCAGGCTGGACCTGGTAGAGCGAA 3487	
QY	783 TGAATAACAGCCCC---GACATCACTGAGGAAAGACTGGAAGCTGGTCACTCTTCA 839	
DB	3488 TGAATAACAGCCCC---GACATCACTGAGGAAAGACTGGAAGCTGGTCACTCTTCA 3547	

QY	840 TTGGGGTCAACGACTTGTGTCTATTTAGATCCGAGGCCCACTTGGCCACGGAAT 899	
DB	3548 TTGGGGTCAACGACTTGTGTCTATTTAGATCCGAGGCCCACTTGGCCACGGAAT 3595	
QY	900 ATGTTTCAGACATCAACAGAGCCCTGGACATCTCTCTGAGGAGCTCCCAAGGGCTTTG 959	
DB	3596 ATGTTTCAGACATCAACAGAGCCCTGGACATCTCTCTGAGGAGCTCCCAAGGGCTTTG 3655	
QY	960 TCAAGCTGTGTGAGTCTATGAGAGTGGCTAGCTGTATACCGGGCAAGGGGGAAATGTG 1019	
DB	3656 TCAAGCTGTGTGAGTCTATGAGAGTGGCTAGCTGTATACCGGGCAAGGGGGAAATGTG 3715	
QY	1020 CNAATGCTGAGCTCAGAACAACTGCACTTGTCTCAGACACTCGCAAAAGCTCCCTGAGA 1079	
DB	3716 CNAATGCTGAGCTCAGAACAACTGCACTTGTCTCAGACACTCGCAAAAGCTCCCTGAGA 3775	
QY	1080 AGCAAGAACTGAAGAAAGTGAACCTGGAACCTCAGCATGGCACTCTTCTCTACT 1139	
DB	3776 AGCAAGAACTGAAGAAAGTGAACCTGGAACCTCAGCATGGCACTCTTCTCTACT 3835	
QY	1140 GGACCAATACACAGAGCTGAGGACTTTGCGGTGTGTGTCAGGCTTTTCTTCAAAACA 1199	
DB	3836 GGACCAATACACAGAGCTGAGGACTTTGCGGTGTGTGTCAGGCTTTTCTTCAAAACA 3895	
QY	1200 CACTCACCCCACTGAACGAGAGAGGGAACACTGACCTTCTTCTCCGAGGACTGTT 1259	
DB	3896 CACTCACCCCACTGAAC--AGAGGGGACACTGACCTTCTTCTCCGAGGACTGTT 3952	
QY	1260 TTCACTTCTCAGACCGGGCATGCCAGATGCCATCGCACTCTGGAACAACATGCTGG 1319	
DB	3953 TTCACTTCTCAGACCGGGCATGCCAGATGCCATCGCACTCTGGAACAACATGCTGG 4012	
QY	1320 AACAGTGGGCGCAGAGACTACCTTCAACAACTTCAACAGCCGAGCCGAACTCAAGT 1379	
DB	4013 AACAGTGGGCGCAGAGACTACCTTCAACAACTTCAACAGCCGAGCCGAACTCAAGT 4072	
QY	1380 GCGCTTCTCTGAGAGCCCTTACCTTACACCTTGCGGAACAGCCGATTTGCTCCAGACC 1439	
DB	4073 GCGCTTCTCTGAGAGCCCTTACCTTACACCTTGCGGAACAGCCGATTTGCTCCAGACC 4132	
QY	1440 AGGCTTGAAGAGACCCCGAGGCTGTCTTATGCGGTGTCTTCCAGTGGCAGCGGAGTGGCC 1499	
DB	4133 AGGCTTGAAGAGACCCCGAGGCTGTCTTATGCGGTGTCTTCCAGTGGCAGCGGAGTGGCC 4192	
QY	1500 TTGTGGTGGGATCATCGGACAGTGTCTGAGGTGCAAGAGAGTGGCCGAGGGAAG 1559	
DB	4193 TTGTGGTGGGATCATCGGACAGTGTCTGAGGTGCAAGAGAGTGGCCGAGGGAAG 4252	
QY	1560 ATCTCTCAATGAGCCTTGGGCACTGTGGCCCTTATAGCCCGGGGGTGGTCTTCACTTAA 1619	
DB	4253 ATCTCTCAATGAGCCTTGGGCACTGTGGCCCTTATAGCCCGGGGGTGGTCTTCACTTAA 4312	
QY	1620 ACTTCCCTATAGGCACTCTTTCACCGCTCTGCCCCAGCCACTCCCGGCCACACAGGACA 1679	
DB	4313 ACTTCCCTATAGGCACTCTTTCACCGCTCTGCCCCAGCCACTCCCGGCCACACAGGACA 4372	
QY	1680 TGCTTCAATGCTGTGGTCCATAGGAAGCCAGGGGACAGTCAAACTTCTTGG 1732	
DB	4373 TGCTTCAATGCTGTGGTCCATAGGAAGCCAGGGGACAGTCAAACTTCTTGG 4425	

RESULT 7

ADN61816

ID ADN61816 standard; cDNA; 4425 BP.

AC ADN61816;

XX 01-JUL-2004 (first entry)

DT Human cDNA encoding NOV24c.

DE Human; ss; gene; NOVX; diabetes; obesity; infectious disease; anorexia;

XX Human; ss; gene; NOVX; diabetes; obesity; infectious disease; anorexia;

KW

KW cancer-associated cachexia; cancer; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW haematopoietic disorder; dyslipidaemia; chronic disease.
 OS Homo sapiens.
 XX US2004043382-A1.
 XX 04-MAR-2004.
 XX 07-MAR-2002; 2002US-00092900.
 XX 08-MAR-2001; 2001US-0274191P.
 XX 08-MAR-2001; 2001US-0274194P.
 PR 08-MAR-2001; 2001US-0274281P.
 PR 08-MAR-2001; 2001US-0274322P.
 PR 09-MAR-2001; 2001US-0274849P.
 PR 12-MAR-2001; 2001US-0275235P.
 PR 13-MAR-2001; 2001US-0275578P.
 PR 13-MAR-2001; 2001US-0275579P.
 PR 13-MAR-2001; 2001US-0275601P.
 PR 14-MAR-2001; 2001US-0276000P.
 PR 16-MAR-2001; 2001US-0276776P.
 PR 19-MAR-2001; 2001US-0276994P.
 PR 20-MAR-2001; 2001US-0277239P.
 PR 20-MAR-2001; 2001US-0277321P.
 PR 20-MAR-2001; 2001US-0277327P.
 PR 20-MAR-2001; 2001US-0277338P.
 PR 21-MAR-2001; 2001US-0277791P.
 PR 22-MAR-2001; 2001US-0277833P.
 PR 23-MAR-2001; 2001US-0278152P.
 PR 26-MAR-2001; 2001US-0278894P.
 PR 27-MAR-2001; 2001US-0278999P.
 PR 27-MAR-2001; 2001US-0279036P.
 PR 28-MAR-2001; 2001US-0279344P.
 PR 30-MAR-2001; 2001US-0279995P.
 PR 30-MAR-2001; 2001US-0280233P.
 PR 02-APR-2001; 2001US-0280802P.
 PR 02-APR-2001; 2001US-0280822P.
 PR 02-APR-2001; 2001US-0280900P.
 PR 04-APR-2001; 2001US-0281444P.
 PR 13-APR-2001; 2001US-0283675P.
 PR 30-APR-2001; 2001US-0287424P.
 PR 02-MAY-2001; 2001US-0288066P.
 PR 03-MAY-2001; 2001US-0288342P.
 PR 03-MAY-2001; 2001US-0288528P.
 PR 15-MAY-2001; 2001US-0291190P.
 PR 16-MAY-2001; 2001US-0291099P.
 PR 16-MAY-2001; 2001US-0291240P.
 PR 30-MAY-2001; 2001US-0294485P.
 PR 31-MAY-2001; 2001US-0294889P.
 PR 31-MAY-2001; 2001US-0294899P.
 PR 18-JUN-2001; 2001US-0299027P.
 PR 19-JUN-2001; 2001US-0299303P.
 PR 19-JUN-2001; 2001US-0299310P.
 PR 10-JUL-2001; 2001US-0304354P.
 PR 31-JUL-2001; 2001US-0309198P.
 PR 16-AUG-2001; 2001US-0312903P.
 PR 10-SEP-2001; 2001US-0318452P.
 PR 12-SEP-2001; 2001US-0318770P.
 PR 27-SEP-2001; 2001US-0325430P.
 PR 27-SEP-2001; 2001US-0325681P.
 PR 18-OCT-2001; 2001US-0330380P.
 PR 31-OCT-2001; 2001US-0335301P.
 PR 14-NOV-2001; 2001US-0332172P.
 PR 14-NOV-2001; 2001US-0332717P.
 PR 14-NOV-2001; 2001US-0332722P.
 PR 14-NOV-2001; 2001US-0333184P.
 PR 14-NOV-2001; 2001US-0333272P.
 PR 21-NOV-2001; 2001US-0332094P.
 PR 03-DEC-2001; 2001US-0337426P.
 PR 03-DEC-2001; 2001US-0338092P.
 PR 04-DEC-2001; 2001US-0337185P.

PR 03-JAN-2002; 2002US-0345705P.

XX (PADI/) PADIGARU M.
 PA (SPYT/) SPYTEK K A.
 PA (SHEN/) SHENOY S G.
 PA (TAUP/) TAUFIER R J.
 PA (PENA/) PENA C E A.
 PA (LILL/) LI L.
 PA (ZERH/) ZERHUSEN B D.
 PA (GUSE/) GUSEV V Y.
 PA (JIWV/) JI W.
 PA (GORM/) GORMAN L.
 PA (MILL/) MILLER C E.
 PA (KEKU/) KEKUDA R.
 PA (PATT/) PATTURAJAN M.
 PA (GANG/) GANGOLLI E A.
 PA (VERN/) VERNET C A M.
 PA (GUOX/) GUO X S.
 PA (TCHE/) TCHERNEV V T.
 PA (FERN/) FERNANDES E R.
 PA (CASM/) CASMAN S J.
 PA (MALY/) MALYANKAR U M.
 PA (GERL/) GERLACH V.
 PA (LIUY/) LIU Y.
 PA (ANDE/) ANDERSON D W.
 PA (SPAD/) SPADERNA S K.
 PA (CATT/) CATTERTON E.
 PA (LEIT/) LEITE M W.
 PA (ZHON/) ZHONG H.
 PA (ALSO/) ALSOBROOK J P.
 PA (LEPL/) LEPLEY D M.
 PA (RIEG/) RIEGER D K.
 PA (BURG/) BURGESS C E.

XX Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L;
 PI Zerrhusen BD, Gusev VY, Ji W, Gorman L, Miller CE, Kekuda R;
 PI Patturajan M, Gangolli EA, Vernet CAM, Guo XS, Tchernev VT;
 PI Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y;
 PI Anderson DW, Spaderna SK, Catterton E, Leite MW, Zhong H;
 PI Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
 XX WPI; 2004-225693/21.
 DR P-PSDB; ADN61817.

XX New NOVX polypeptides and nucleic acid molecules useful for diagnosing,
 PT preventing or treating NOVX-associated disorders, e.g. cancer, diabetes,
 PT infection or obesity, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.

XX Claim 17; SEQ ID NO 85; 786pp; English.

XX The invention relates to an isolated polypeptide (designated NOVX, or
 CC NOV1-NOV127) comprising a sequence selected from 178 fully defined amino
 CC acid sequences (and their mature forms, variants and fragments). Also
 CC included are an isolated nucleic acid molecule encoding NOVX, a vector
 CC comprising the nucleic acid, a cell comprising the vector, methods for
 CC determining the presence or amount of the polypeptide or the nucleic acid
 CC molecule in a sample, methods for determining the presence of or
 CC predisposition to a disease associated with altered levels of expression
 CC of the above polypeptide or nucleic acid molecule in a first mammalian
 CC subject, a method for identifying an agent that binds to the above
 CC polypeptide, a method for identifying a potential therapeutic agent for
 CC use in the treatment of a pathology that is related to aberrant
 CC expression or physiological interactions of the polypeptide, a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide and a method for modulating
 CC the activity of the polypeptide cited above. The composition and methods
 CC are useful for diagnosing, preventing or treating diseases such as
 CC diabetes, obesity, infectious diseases, anorexia, cancer-associated
 CC cachexia, cancer, neurodegenerative disorders like Alzheimer's disease or
 CC Parkinson's disease, immune disorders, haematopoietic disorders,
 CC dyslipidaemias, and other chronic diseases. These may also be used in
 CC chromosome mapping, tissue typing, preventive medicine and

Mon Mar 28 09:43:24 2005

CC	pharmacogenomics. The polypeptides are also useful as vaccines. The	
CC	present sequence encodes a NOVX protein of the invention.	
XX		
SQ	Sequence 4425 BP; 1083 A; 1254 C; 1163 G; 924 T; 0 U; 1 Other;	
Query Match	77.3%; Score 1417.8; DB 12; Length 4425;	
Best Local Similarity	88.5%; Pred. No. 0;	
Matches 1693; Conservative	0; Mismatches 12; Indels 208; Gaps 6;	
1	CTGACGCCAATTTGTTGACCAATCTCCGCAATGCTTGGAGCTCTGTCATAGAGAGCTTT 60	
2540	CTGACGCCAATTTGTTGACCAATCTCCGCAATGCTTGGAGCTCTGTCATAGAG 2593	
61	TCCTTTAGGTGCCAGAGTCTTGCTCAACCTCGTGGACTTCTGAAACCCCACTATGTC 120	
2594	-----AGTGGCCAGAGTCTTGCTCAACCTCGTGGACTTCTGAAACCCCACTATGTC 2647	
121	GGCAGGTGTTCTGGGAAACCCAGACAGTGGCCAGTGCAGCAGG-----165	
2648	GGCAGGTGTTCTGGGAAACCCAGACAGTGGCCAGTGCAGCAGGCGGTTTGTGTA 2707	
166	-----165	
2708	ACTGGTCTGACCTCGGGAGAACTCCCAAGAGCTAGCCAGGCTGGAGGCTTCAGCC 2767	
166	-----CCAGAGCAGATGGCGAGCTGGTGGGTGAGGCTCAGGCGCTATGACAGCAGGAGG 218	
2768	GACCTACAGAGCAGATGGCGAGCTGGTGGGTGAGGCTCAGGCGCTATGACAGCAGGAGG 2827	
219	ACTTCTCTGCTGCTGAGCGCTTCTTCCAGAACTCCAGTCCCTGCTCCTG 271	
2828	ACTTCTCTGCTGCTGAGCGCTTCTTCCAGAACTCCAGTCCCTGCTCCTGCGAGTG 2887	
272	-----271	
2888	GGCTCCAGATAGCTCTTCTTTGCCCCAGAGCTGCATCCACCACCAATCAGAAATTCAC 2947	
272	-----GGCTTGAACCACTTGGAGGAGCAACAGAGAG 302	
2948	CCAGCTGGCCAGAGCCCTTTGGACCAATATGCTTGAACCACTTGGAGGAGCAACAGAG 3007	
303	CCCTGACCTGAGAGAGATGCCCATCACTGCTCCCACTCAGAAATGAGCCCTTCTGA 362	
3008	CCCTGACCTGAGAGAGATGCCCATCACTGCTCCCACTCAGAAATGAGCCCTTCTGA 3067	
363	GRACCCCTGGATAGTAACTACAGTACCCCATCAAGCGGCCATTTGAGAACTGGGSCA 422	
3068	GRACCCCTGGATAGTAACTACAGTACCCCATCAAGCGGCCATTTGAGAACTGGGSCA 3127	
423	GTGACTTCTGTTGACAGAGTGAAGCTTCCCAATAGTGTTCACACCTCTGTCCACCAAGC 482	
3128	GTGACTTCTGTTGACAGAGTGAAGCTTCCCAATAGTGTTCACACCTCTGTCCACCAAGC 3187	
483	TCGACACAGAGAGATCAAAAGTGGTGGCGCCCTGGTGAATCTGTGACTACAGCAGTGG 542	
3188	TCCACACAGAGAGATCAAAAGTGGTGGCGCCCTGGTGAATCTGTGACTGGCAGTGG 3247	
543	GAGCTTCGACCAAAACAACTCCAGTACCTACCACTCTGGAGGGAGCTCTCTGGAGCA 602	
3248	GAGCTTCGACCAAAACAACTCCAGTACCTACCACTCTGGAGGGAGCTCTCTGGAGCA 3307	
603	TTGGAGGGAGTGGGAACTTGGAGACTCACACCACTGTCGCCCAATCTTGAAGAAATCA 662	
3308	TTGGAGGGAGTGGGAACTTGGAGACTCACACCACTGTCGCCCAATCTTGAAGAAATCA 3367	
663	ACCTTACCTCTTGGCTTCTTACAGAGCTGGGAGGAGCAGAGGACTAAATGTGG 722	
3368	ACCTTACCTCTTGGCTTCTTACAGAGCTGGGAGGAGCAGAGGACTAAATGTGG 3427	
723	CAGCGGAGGGGCCAGAGCTAGGGACATGCCAGGCCCAAGGCTGGTAGGGGA 782	
3428	CAGCGGAGGGGCCAGAGCTAGGGACATGCCAGGCCCAAGGCTGGTAGGGGA 3487	

QY	783	TGAAAAACAGCCCC---GACATCAACCTCGAGAAAGACTGGAGCTGGTTCACACTTCTCA 839
Db	3488	TGAAAAACAGCCCCCAGGACATCAACCTCGAGAAAGACTGGAGCTGGTTCACACTTCTCA 3547
QY	840	TTGGGGTCAACGACTTGTGTCAITACTTGTGAGAAATCCGAGGCCCACTTGGCCACCGAAT 899
Db	3548	TTGGGGTCAACGACTTGTGTCAITACTTGTGAGAAATCCGAGGCCCACTTGGCCACCGAAT 899
QY	900	ATGTTTACGACATCAACAGGCCCTTGAACATCTCTCTGAGGAGCTCCCAAGGGCTTTCG 959
Db	3596	ATGTTTACGACATCAACAGGCCCTTGAACATCTCTCTGAGGAGCTCCCAAGGGCTTTCG 3655
QY	960	TCAAAGTGGTGGAGTCAATGAGCTGGCTAGCTGTATACCTGTATACAGGGCAAGGGGAAATGTG 1019
Db	3656	TCAAAGTGGTGGAGTCAATGAGCTGGCTAGCTGTATACCTGTATACAGGGCAAGGGGAAATGTG 3715
QY	1020	CCATGCTGCGAGCTCAGAAACAACTGCACTTGGCTCAGACACTCGCAAGTCTCCCTCGAGA 1079
Db	3716	CCATGCTGCGAGCTCAGAAACAACTGCACTTGGCTCAGACACTCGCAAGTCTCCCTCGAGA 3775
QY	1080	AGCAAGAACTGAAGAAAGTGAACCTGAAACCTCCAGCATGGCATCTCCAGTTTCTCTACT 1139
Db	3776	AGCAAGAACTGAAGAAAGTGAACCTGAAACCTCCAGCATGGCATCTCCAGTTTCTCTACT 3835
QY	1140	GGCAACCAATACACACAGCGTGAAGACTTTGCGGTTGTGTCAGCCTTCTTCCAAAAACA 1199
Db	3836	GGCAACCAATACACACAGCGTGAAGACTTTGCGGTTGTGTCAGCCTTCTTCCAAAAACA 3895
QY	1200	CACCTACCCCACTGAACGAGAGAGAGGAGCACTGACCTCACTTCTTCCGAGGACTGTT 1259
Db	3896	CACCTACCCCACTGAAC--AGAGGGGACACTGACCTCACTTCTTCCGAGGACTGTT 3952
QY	1260	TTCACTTCTCAGACCCGCGGCGATGCCAGATGGCCATCCACTCTGGAACAAACATGCTGG 1319
Db	3953	TTCACTTCTCAGACCCGCGGCGATGCCAGATGGCCATCCACTCTGGAACAAACATGCTGG 4012
QY	1320	AACAGTGGGCGCAAGACTTACCTCCAAACAACTTCCACCAAGCCAGCCAACTCAAGT 1379
Db	4013	AACAGTGGGCGCAAGACTTACCTCCAAACAACTTCCACCAAGCCAGCCAACTCAAGT 4072
QY	1380	GCCCCCTCTCTGAGAGCCCTTACCTCTACACCTGGGGAACAGCCGATTTGCTCCAGACC 1439
Db	4073	GCCCCCTCTCTGAGAGCCCTTACCTCTACACCTGGGGAACAGCCGATTTGCTCCAGACC 4132
QY	1440	AGGCTGAAGAGAGCCCGGAGGTGTCTACTTGGGCTGTCCAGTGGGAGCGGGAGTGGCC 1499
Db	4133	AGGCTGAAGAGAGCCCGGAGGTGTCTACTTGGGCTGTCCAGTGGGAGCGGGAGTGGCC 4192
QY	1500	TTGTGGTGGGCATCATTCGGGACAGTGTCTGGAGTGCAGGAGAGTGGCGGAGGGAAG 1559
Db	4193	TTGTGGTGGGCATCATTCGGGACAGTGTCTGGAGTGCAGGAGAGTGGCGGAGGGAAG 4252
QY	1560	ATCCTCAATGAGCCTGGCAGCTGTGGCCCTCTAGGCCCGGGGGTGGTCTTCACTTAA 1619
Db	4253	ATCCTCAATGAGCCTGGCAGCTGTGGCCCTCTAGGCCCGGGGGTGGTCTTCACTTAA 4312
QY	1620	ACTTCCCTATAGCCACTTCTTCAACCGCCCTCTGCCCCCAGCCACTCCCGGCCACAGGACA 1679
Db	4313	ACTTCCCTATAGCCACTTCTTCAACCGCCCTCTGCCCCCAGCCACTCCCGGCCACAGGACA 4372
QY	1680	TGCTTCAATGCTGTGGCAGTATAGGAGCCAGGAGCCAGGGGACAGTCAAACTTCTGG 1732
Db	4373	TGCTTCAATGCTGTGGTGGCCATAGGAGCCAGGAGCCAGGGGACAGTCAAACTTCTGG 4425

RESULT 8
ADOL18836
ID ADOL18836 standard; DNA; 4508 BP.
XX
AC ADOL18836;
XX
DT 12-AUG-2004 (first entry)
XX

Human lipid-associated molecule (LIPAM) gene SeqID31.

lipid-associated molecule; LIPAM; neuroprotective; relaxant; antithyroid;
antidiabetic; cytosolic; dermatological; immunosuppressive;
antiinflammatory; thyromimetic; antiallergic; neurotrophic; anticonvulsant;
gastrointestinal; hepatotropic; nephrotropic; fungicide; protozoacide;
antiparkinsonian; antibacterial; antiparasitic; cardiant; cardiovascular; anti-HIV;
virucide; uropathic; antirheumatic; Crohn's disease; renal disorder;
neurotropic; LIPAM agonist; LIPAM antagonist; Gene therapy;
neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
muscular disorder; myotonic dystrophy; catatonia; endocrine disorder;
Grave's disease; cancer; leukemia; cervical; breast cancer;
immunological disorder; scleroderma; systemic lupus erythematosus;
allergy; gastrointestinal disorder; Crohn's disease; renal disorder;
Goodpasture's syndrome; infection; viral; bacterial; fungal; parasitic;
protozoal; helminthic; cardiovascular disorder; atherosclerosis;
hepatic disease; cirrhosis; transgenic animal; gene; ds; human.

Homo sapiens.

WO2004041165-A2.

27-MAY-2004.

10-NOV-2003; 2003WO-US035946.

13-NOV-2002; 2002US-0426105P.

12-DEC-2002; 2002US-0433215P.

07-MAR-2003; 2003US-0453127P.

13-MAR-2003; 2003US-0454801P.

24-APR-2003; 2003US-0465495P.

24-APR-2003; 2003US-0465619P.

01-AUG-2003; 2003US-0491800P.

(INCY-) INCYTE CORP.

Jiang X, Becha SD, Bulloch SA, Chang H, Chawla NK, Elliott VS;
Emerling BM, Gietzen KJ, Hafalia AJA, Jackson AA, Kable AE, Khare R;
Lee SY, Marquis JP, Murage J, Swarnakar A, Yang YG;

WPI; 2004-420307/39.

P-PSDB; ADOI8815.

New LIPAM polypeptides, useful for diagnosing, preventing, and treating
disorders associated with abnormal expression or activity of LIPAM, e.g.
neuromuscular, immunological, cardiovascular disorders, cancer and/or
infections.

Claim 5; SEQ ID NO 31; 207pp; English.

This invention relates to novel human lipid-associated molecules (LIPAM)
and the DNA sequences which encode them. The invention may be useful for
the production of compounds with a neuroprotective, relaxant,
antithyroid, antidiabetic, cytosolic, dermatological, immunosuppressive,
antiinflammatory, thyromimetic, antiallergic, neurotrophic, anticonvulsant,
gastrointestinal, hepatotropic, nephrotropic, fungicide, protozoacide,
antiparkinsonian, antibacterial, antiparasitic, cardiant, cardiovascular,
virucide, uropathic, antirheumatic, Crohn's disease, renal disorder;
neurotropic activity acting as LIPAM agonists or antagonists. In addition,
the disclosed sequences may be useful for gene therapy. The invention may
be useful for diagnosing, preventing, and treating disorders associated
with an abnormal expression or activity of LIPAM, such as
neurodegenerative disorders (for example Parkinson's disease, Alzheimer's
disease), muscular disorders (for example myotonic dystrophy, catatonia),
endocrine disorders (for example diabetes, Grave's disease), cancers (for
example leukemia, cervical or breast cancer), immunological disorders
(for example scleroderma, systemic lupus erythematosus, allergies),
gastrointestinal disorders (for example Crohn's disease), renal disorders
(for example Goodpasture's syndrome), infections (for example viral,
bacterial, fungal, parasitic, protozoal, helminthic) cardiovascular
disorders (for example atherosclerosis), or hepatic diseases (for example
cirrhosis). LIPAM or its fragments may also be used in screening for
compounds that specifically bind to and modulate the activity of LIPAM.

CC The polynucleotides can be used to create humanised animals or transgenic
CC animals to model human disease. The present sequence is that of a human
CC lipid-associated molecule (LIPAM) gene of the invention.

XX Sequence 4508 BP; 1108 A; 1256 C; 1190 G; 954 T; 0 U; 0 Other;

Query Match 76.3%; Score 1400; DB 12; Length 4508;

Best Local Similarity 86.5%; Pred. No. 0;

Matches 1705; Conservative 0; Mismatches 0; Indels 265; Gaps 4;

Qy 1 CTGCAGCAACTTTGTTGACCATCTCCGCAATCGCTGGAGCTCTGCATAGAGAGCTTT 60

Db 2626 CTGCAGCAACTTTGTTGACCATCTCCGCAATCGCTGGAGCTCTGCATAGAG----- 2679

Qy 61 TCCCTTAGGTGCCAGAGTCTCTGCTCAACCTCGTGGACTTCTCAACCCCACTATCATGC 120

Db 2680 -----AGGTGCCAGAGTCTCTGCTCAACCTCGTGGACTTCTCAACCCCACTATCATGC 2733

Qy 121 GGCAGGTGTTCTTGGGAAACCCAGACAAGTGCCAGTGCAGCAGGCCA----- 168

Db 2734 GGCAGGTGTTCTTGGGAAACCCAGACAAGTGCCAGTGCAGCAGGCCA----- 2793

Qy 169 ----- 168

Db 2794 ACTGCGTTCTGACCTCGGGAGAACTCCCAAGAGTAGCCAGGCTGGAGCCTTCAGCC 2853

Qy 169 -----GAGCAGCATGCGCAGCTGGTGGGGTTCAGGCCGTATGACACGAGGAGG 218

Db 2854 GAGCCTACCGAGCAGCATGCGCAGCTGGTGGGGTTCAGGCCGTATGACACGAGGAGG 2913

Qy 219 ACTTCTCTGTGGTCTGCAGCCCTTTTCCAGACAATCCAGCTCCCTGTCTCTGGC----- 273

Db 2914 ACTTCTCTGTGGTCTGCAGCCCTTTTCCAGACAATCCAGCTCCCTGTCTCTGGCGATG 2973

Qy 274 ----- 273

Db 2974 GGCCTCCAGATAGTCTCTTTTGGCCCCAGACTGCATCCACCCAAATCAGAAATTCCTACT 3033

Qy 274 -----GCTTGAACCACTTGGGAAGCAAAACAGAGA 302

Db 3034 CCCAGCTGGCCAGAGCCCTTTGGACCAATATGCTTGAACCACTTGGGAAGCAAAACAGAGA 3093

Qy 303 CCCTGGACCTGAGACAGAGATGCCATCACTGTCCCCTCCTCAGAAATGAGCCCTTCCTGA 362

Db 3094 CCCTGGACCTGAGACAGAGATGCCATCACTGTCCCCTCCTCAGAAATGAGCCCTTCCTGA 3153

Qy 363 GAACCCCTCGGAATAGTAACCTACAGTACCCCATCAAGCCAGCCATTGAGAACTGGGGCA 422

Db 3154 GAACCCCTCGGAATAGTAACCTACAGTACCCCATCAAGCCAGCCATTGAGAACTGGGGCA 3213

Qy 423 GTGACTTCTGTGTACAGAGTGGGAAGCTTCCAAATAGTTTCCAACTCTGTCCACAGC 482

Db 3214 GTGACTTCTGTGTACAGAGTGGGAAGCTTCCAAATAGTTTCCAACTCTGTCCACAGC 3273

Qy 483 TCCGACACGACAGCATCAAAAGTGTGTGGCCCGCTTGGGTGACTCTCTGACTACAGCAGTGG 542

Db 3274 TCCGACACGACAGCATCAAAAGTGTGTGGCCCGCTTGGGTGACTCTCTGACTACAGCAGTGG 3333

Qy 543 GAGCTCGACCAAACTCCAGTGCATCCACATCTTGGAGGGGACTCTCTTGGAGCA 602

Db 3334 GAGCTCGACCAAACTCCAGTGCATCCACATCTTGGAGGGGACTCTCTTGGAGCA 3393

Qy 603 TTGGAGGGGATGGGAACCTGGAGACTCACACCACTGCCCAACTTCTGAAGAAGTTCA 662

Db 3394 TTGGAGGGGATGGGAACCTGGAGACTCACACCACTGCCCAACTTCTGAAGAAGTTCA 3453

Qy 663 ACCCTTACCTCTCTGGCTTCTCTACAGCACTCTGGAGGGGACAGCAGGACTTAAATGTGG 722

Db 3454 ACCCTTACCTCTCTGGCTTCTCTACAGCACTCTGGAGGGGACAGCAGGACTTAAATGTGG 3513

Qy 723 CAGCGGAAGGGGCAGAGCTAGGGAATGCGAGCCCAAGGCTTGGGACTTGTAGAGCGAA 782

Db 3514 CAGCGGAAGGGGCAGAGCTAGGGAATGCGAGCCCAAGGCTTGGGACTTGTAGAGCGAA 3573

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Mon Mar 28 09:43:24 2005

QY	783	TGAAAAACAGCCCGACATCAACCTGGAGAAAGACTGGAAGCTGGTCACTCTTCAATTG	842	XX	AC	ABX97050;
Db	3574	TGAAAAACAGCCCGACATCAACCTGGAGAAAGACTGGAAGCTGGTCACTCTTCAATTG	3633	XX	XX	20-MAY-2003 (first entry)
QY	843	GGGTCAACGACTTGTGTCAATTAATCTGTGAATCCGGAGCCCACTTGGCCACGGAATATG	902	DE	Human NOV24c cDNA.	
Db	3634	GGGTCAACGACTTGTGTCAATTAATCTGTGAATCCGGAGCCCACTTGGCCACGGAATATG	3693	XX	NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;	
QY	903	TTTACGACATCCAAACAGCCCTGGACATCTCTGTGAGAGCTCCCAAGGCTTTTGTCTCA	962	KW	hypotensive; cardiomyopathy; Bronchial asthma; gene therapy; vaccine;	
Db	3694	TTTACGACATCCAAACAGCCCTGGACATCTCTGTGAGAGCTCCCAAGGCTTTTGTCTCA	3753	KW	human; gene; ss.	
QY	963	ACGTGGTGGAGGTCAATGGAGCTGGTGTACAGGGCCCAAGCGGGAATGTGCCA	1022	OS	Homo sapiens.	
Db	3754	ACGTGGTGGAGGTCAATGGAGCTGGTGTACAGGGCCCAAGCGGGAATGTGCCA	3813	XX	WO200272757-A2.	
QY	1023	TGCTGGAGCTCAGACACACTGCTTGGCTCAGACACTCGCAAAAGCTCCCTGGAGAAGC	1082	XX	19-SEP-2002.	
Db	3814	TGCTGGAGCTCAGACACACTGCTTGGCTCAGACACTCGCAAAAGCTCCCTGGAGAAGC	3873	XX	08-MAR-2002; 2002WO-US006908.	
QY	1083	AAGAACTGAAGAAAGTGAATGAACTCGAGATCGGATCTCCAGTTTCTCTACTTGGC	1142	XX	08-MAR-2001; 2001US-0274101P.	
Db	3874	AAGAACTGAAGAAAGTGAATGAACTCGAGATCGGATCTCCAGTTTCTCTACTTGGC	3933	XX	08-MAR-2001; 2001US-0274194P.	
QY	1143	ACCAATACACACAGCTGAGGACTTTGCGGTGTGTGTCAGCCCTTTCTTCCAAAACACAC	1202	XX	08-MAR-2001; 2001US-0274281P.	
Db	3934	ACCAATACACACAGCTGAGGACTTTGCGGTGTGTGTCAGCCCTTTCTTCCAAAACACAC	3993	XX	08-MAR-2001; 2001US-0274322P.	
QY	1203	TCACCCCACTGAACGAGAGAGGGGACACTGACCTTCTTCTCGAGGACTGTTTTC	1262	XX	09-MAR-2001; 2001US-0274849P.	
Db	3994	TCACCCCACTGAACGAGAGAGGGGACACTGACCTTCTTCTCGAGGACTGTTTTC	4053	XX	12-MAR-2001; 2001US-0275235P.	
QY	1263	ACTTCTCAGACGCGGGGATGCGGAGATGGCCATCGCACTCTGGAACACATG	4106	XX	13-MAR-2001; 2001US-0275578P.	
Db	4054	ACTTCTCAGACGCGGGGATGCGGAGATGGCCATCGCACTCTGGAACACATG	4106	XX	13-MAR-2001; 2001US-0275601P.	
QY	1323	CAGTGGGGCGGAAGACTACTCTCCACAACTTCAACCCACAGCGGACCAACTCAATGCC	1382	XX	13-MAR-2001; 2001US-0276000P.	
Db	4107	CAGTGGGGCGGAAGACTACTCTCCACAACTTCAACCCACAGCGGACCAACTCAATGCC	4106	XX	14-MAR-2001; 2001US-0276767P.	
QY	1383	CCTTCTCAGAGCCCTTACTCTACACCTGCGGAACAGCCGATGCTCCAGACAGG	1442	XX	16-MAR-2001; 2001US-0276994P.	
Db	4107	CCTTCTCAGAGCCCTTACTCTACACCTGCGGAACAGCCGATGCTCCAGACAGG	4158	XX	19-MAR-2001; 2001US-0277321P.	
QY	1443	CTGGAAGCCCGCCAGGTGCTCTACTGGGCTGTCCAGTGGCAGCGGAGTCCGCTTG	1502	XX	20-MAR-2001; 2001US-0277327P.	
Db	4159	CTGGAAGCCCGCCAGGTGCTCTACTGGGCTGTCCAGTGGCAGCGGAGTCCGCTTG	4218	XX	21-MAR-2001; 2001US-0277791P.	
QY	1503	TGTTGGGCTATCTCGGACAGTGGTCTGAGGTGCGAGAGGTGGCCGGAGGAATC	1562	XX	22-MAR-2001; 2001US-0278333P.	
Db	4219	TGTTGGGCTATCTCGGACAGTGGTCTGAGGTGCGAGAGGTGGCCGGAGGAATC	4278	XX	23-MAR-2001; 2001US-0278152P.	
QY	1563	CTCCATAGCCCTGCGCACTGTGGCCCTCTAGGCCCGGGGGTGGTCTCACCCTAACT	1622	XX	26-MAR-2001; 2001US-0278894P.	
Db	4279	CTCCATAGCCCTGCGCACTGTGGCCCTCTAGGCCCGGGGGTGGTCTCACCCTAACT	4338	XX	27-MAR-2001; 2001US-0279036P.	
QY	1623	CCCTATAGCCCTTCTTACCGCCCTCTGCCCGCCCACTCCCGCCCAACAGGACATGC	1682	XX	28-MAR-2001; 2001US-0279344P.	
Db	4339	CCCTATAGCCCTTCTTACCGCCCTCTGCCCGCCCACTCCCGCCCAACAGGACATGC	4398	XX	30-MAR-2001; 2001US-0279955P.	
QY	1683	TTCAATGCTGGTGGCATTAGGAAGCCAGGGGACAGTCAAACTTCTGGGGCTGGCT	1742	XX	30-MAR-2001; 2001US-0280233P.	
Db	4399	TTCAATGCTGGTGGCATTAGGAAGCCAGGGGACAGTCAAACTTCTGGGGCTGGCT	4458	XX	02-APR-2001; 2001US-0280822P.	
QY	1743	TCTTCCAGGCTATGCTCTCGAATGATATTAATTAATTAATTAATTAATTAATTAAT	1792	XX	02-APR-2001; 2001US-0280900P.	
Db	4459	TCTTCCAGGCTATGCTCTCGAATGATATTAATTAATTAATTAATTAATTAATTAAT	4508	XX	04-APR-2001; 2001US-0281194P.	

RESULT 9
ABX97050
ID ABX97050 standard; cDNA; 4425 BP.

PR 14-NOV-2001; 2001US-0332272P.
 PR 14-NOV-2001; 2001US-0333184P.
 PR 14-NOV-2001; 2001US-0333272P.
 PR 21-NOV-2001; 2001US-0332094P.
 PR 03-DEC-2001; 2001US-0337426P.
 PR 03-DEC-2001; 2001US-0338092P.
 PR 04-DEC-2001; 2001US-0337185P.
 PR 03-JAN-2002; 2002US-0345705P.
 PR 07-MAR-2002; 2002US-00092900.
 XX (CURA-) CURAGEN CORP.
 PA Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L;
 XX Zerkhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;
 PI Patturajan M, Gangolli E, Vernet CAM, Guo X, Tchernev V;
 PI Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
 PI Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobrook JP;
 PI Lopley DM, Rieger DK;
 XX WPI; 2002-723332/78.
 DR P-PSDB; ABU65083.
 XX
 PT NOVX polypeptides and polynucleotides, useful for preventing or treating
 PT a disorder associated with aberrant NOVX expression or activity e.g.,
 PT cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
 PT asthma.
 XX
 PS Claim 13; Page 169-170; 1103pp; English.
 XX
 PS This invention describes novel human NOVX polypeptides which have
 CC cytosolic, cardiac, antiarteriosclerotic, antiasthmatic and hypotensive
 CC activity. Pharmaceutical compositions comprising the NOVX proteins or
 CC nucleic acid molecules or NOVX antibodies are useful for preventing or
 CC treating a disorder associated with aberrant NOVX expression or activity
 CC e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
 CC asthma. The products of the invention can be used for gene therapy or in
 CC a vaccine. ABX97008-ABX97185 are cDNA fragments amplified and isolated by
 CC the PCR primers and probes represented in ABX13460-ABX13462 and ABX97186-
 CC ABX97593. ABX97008-ABX97185 encode the NOVX proteins described in
 CC ABU65041-ABU65218
 XX
 XX Sequence 4425 BP; 1089 A; 1242 C; 1173 G; 921 T; 0 U; 0 Other;
 SQ

Query Match 74.9%; Score 1374.6; DB 6; Length 4425;
 Best Local Similarity 87.1%; Pred. No. 0;
 Matches 1666; Conservative 0; Mismatches 39; Indels 208; Gaps 6;
 1 CTGCAGCCAACTTTGTTGACCATCTCCGCAATGCTTGGAGCTCCTGCATAGAGCTTT 60
 2540 CTGCAGCCAACTTTGTTGACCATCTCCGCAATGCTTGGAGCTCCTGCATAGAG- 2593
 61 TCCCTTAGGTGCCAGAGTCTGTGTAACCTCGTGGACTTCTGAAACCCCACTATATGC 120
 2594 -----AGGTGCCAGAGTCTGTGTAACCTCGTGGACTTCTGAAACCCCACTATATGC 2647
 121 GGCAGGTGTTCTCTGGGAAACCCAGCAAGTGCCAGTGCAGCAGG----- 165
 2648 GGCAGGTGTTCTCTGGGAAACCCAGCAAGTGCCAGTGCAGCAGGCTTTGTGTA 2707
 166 ----- 165
 2708 ACTCGTCTTACCCCTCGGGGAGAACTCCCAAGAGCTAGCCAGGCTGGAGCCCTTCAGCC 2767
 166 -----CCAGAGCAGATCGGAGCTGTGGGTGAGCCCGCTATGACACCGAGGAG 218
 2768 GAGCCTACCAAGAGCAGATCGGAGCTGTGGGTGAGCCCGCTATGACACCGAGGAG 2827
 219 ACTTCTGTGGTCTGCAGCCCTTTCTCCAGAACATCCAGCTCCCTGTCTCTG 271
 2828 ACTTCTGTGGTCTGCAGCCCTTTCTCCAGAACATCCAGCTCCCTGTCTCTG 2887
 272 ----- 271

Db 2888 GGCTCCAGATACGTCTTCTTTTCCCCAGAGTCATCCACCCAAATCAGAAATTCCTACT 2947
 Qy 272 -----GGCTTTGAACCACTTTGGAGCAAAACAGAGA 302
 Db 2948 CCNAGCTGGCCAGAGCCCTTTGGACCAATATGCTTGAACCACTTTGGAGCAAAACAGAGA 3007
 Qy 303 CCCTGGACCTTGAGAGCAGAGATGCCATACCTGTGCCACTCAGAATGAGCCCTTCTCTGA 362
 Db 3008 CCCTGGACCTTGAGAGCAGAGATGCCATACCTGTGCCACTCAGAATGAGCCCTTCTCTGA 3067
 Qy 363 GAACCCCTCGGAATAGTAACCTACAGTACCCCACTCAAGCCAGCCATTTGAGAACTTGGGGCA 422
 Db 3068 GAACCCCTCGGAATAGTAACCTACAGTACCCCACTCAAGCCAGCCATTTGAGAACTTGGGGCA 3127
 Qy 423 GTGACTTCTGTGTACAGAGTGGAGGCTTCCAAATAGTGTTCCAACCTCTGTCCACAGC 482
 Db 3128 GTGACTTCTGTGTACAGAGTGGAGGCTTCCAAATAGTGTTCCAACCTCTGTCCACAGC 3187
 Qy 483 TCCGACCCAGCAGACATCAAAAGTGGTGGCCGCTTGGGTGACTCTCTGACTACAGAGTGG 542
 Db 3188 TCCGACCCAGCAGACATCAAAAGTGGTGGCCGCTTGGGTGACTCTCTGACTGTCGAGTGG 3247
 Qy 543 GAGCTCGAACCAAACTCCAGTGACCTACCCACATCTTGGAGGGGACTCTCTTGGAGCA 602
 Db 3248 GAGCTCGAACCAAACTCCAGTGACCTACCCACATCTTGGAGGGGACTCTCTTGGAGCA 3307
 Qy 603 TTGGAGGGGATGGGAACCTTGGAGACTCACACCACTGCCCAACTTCTGAAGAAGTTCA 662
 Db 3308 TTGGAGGGGATGGGAACCTTGGAGACTCACACCACTGCCCAACTTCTGAAGAAGTTCA 3367
 Qy 663 ACCCTTACCTCTCTTGGCTTCTTACAGCACTTGGAGGGGACAGAGGACTTAAATGTGG 722
 Db 3368 ACCCTTACCTCTCTTGGCTTCTTACAGCACTTGGAGGGGACAGAGGACTTAAATGTGG 3427
 Qy 723 CAGCGNAGGGCCAGAGCTAGGGACATGCGAGCCAGGCTTGGGACTTGTAGAGCGAA 782
 Db 3428 CAGCGNAGGGCCAGAGCTAGGGACATGCGAGCCAGGCTTGGGACTTGTAGAGCGAA 3487
 Qy 783 TGAATAACAGCCCCC-----GACATCAACCTGGAGAAAGACTCGAAGCTGTCACACTTCA 839
 Db 3488 TGAATAACAGCCCCCAGGACATCAACCTGGAGAAAGACTCGAAGCTGTCACACTTCA 3547
 Qy 840 TTGGGTCAACGACTTGTGTCTTACTGTGAGAAATCCGAGGGCCCACTTGGCCACGGAAT 899
 Db 3548 TTGGGTCAACGACTTGTGTCTTACTGTGAGAAATCCGAGGGC-----GAAT 3595
 Qy 900 ATGTTGAGCAGATCCAAAGCCCTTGGACATCTCTCTGAGGAGCTCCCAAGGCTTTTCG 959
 Db 3596 ATGTTGAGCAGATCCAAAGCCCTTGGACATCTCTCTGAGGAGCTCCCAAGGCTTTTCG 3655
 Qy 960 TCAACGTGGTGGAGGTCATGGAGCTGTAGCTGTACACAGGGCCAAAGGGGAAATGTG 1019
 Db 3656 TCAACGTGGTGGAGGTCATGGAGCTGTAGCTGTACACAGGGCCAAAGGGGAAATGTG 3715
 Qy 1020 CCATGCTGGAGCTCAGAAACAACTTGGCTTCCCTCAGACACTCGCAAAGCTTCCCTGGAGA 1079
 Db 3716 CCATGCTGGAGCTCAGAAACAACTTGGCTTCCCTCAGACACTCGCAAAGCTTCCCTGGAGA 3775
 Qy 1080 AGCAAGAACTGAAGAAAGTGAACCTGGAACCTCCAGCATGCACTCCAGTTTCTCTACT 1139
 Db 3776 AGCAAGAACTGAAGAAAGTGAACCTGGAACCTCCAGCATGCACTCCAGTTTCTCTACT 3835
 Qy 1140 GGCAACCAATACACAGCGGTGAGGACTTTTCGGTGTGGTGCAGCTTTTTCCAAACA 1199
 Db 3836 GGCAACCAATACAGCACTGCACTTGCCTCAGACACTCGCAAAGCTTCCCTTCCAAACA 3895
 Qy 1200 CACTCACCCCACTGAACGAGAGGGGACACTGACCTCCTTCTTCCGAGGACTGTT 1259
 Db 3896 CACTCACCCCACTGAAC--AGAGGGGACACTGACCTCCTTCTTCCGAGGACTGTT 3952
 Qy 1260 TTCACTTCTCAGACCGGGGCATGCCGAGATGGCCATCGCACTCTGGAACCAAGTCTGG 1319
 Db 3953 TTCACTTCTCAGACCGGGGCATGCCGAGATGGCCATCGCACTCTGGAACCAAGTCTGG 4012

Mon Mar 28 09:43:24 2005

Polynucleotides encoding human lipases that are structurally related to animal lipases, particularly phospholipase B, useful for drug screening, diagnosis and in gene therapy of biological disorders.

Claim 1; Page 36-37; 44pp; English.

The invention relates to a novel human lipase (NHL; ABB09555, ABB09556) and to nucleic acids encoding it (AB077623, AB077624). The NHL has structural similarity with animal lipases, particularly phospholipase B. Polynucleotides encoding NHL were obtained using human genomic sequences in conjunction with human thyroid and brain cDNAs. The NHL gene is located on chromosome 2, and contains a C/T polymorphism at position 3953 of the open reading frame (ORF), resulting in an Ala/Val substitution at position 1318 in the protein. NHL nucleotides and proteins are useful for treating disorders such as inflammatory or proliferative disease, infectious disease, clotting disorders, and cancer. They can also be used in screening for compounds useful in the treatment of mental, biological or medical disorders, as diagnostic reagents, in clinical trials monitoring and in cosmetic and nutritional applications. NHL nucleotides can additionally be used in the detection of disease-associated mutations, in the analysis of gene expression, for the recombinant expression of NHL, to generate transgenic animals, in gene therapy, and as part of ribozyme and/or triple helix sequences useful in the modulation of NHL gene expression. The present sequence represents the cDNA encoding the Ala 1318 variant of NHL.

Sequence 4377 BP; 1085 A; 1217 C; 1155 G; 920 T; 0 U; 0 Other;

Query Match 74.2%; Score 1362; DB 6; Length 4377;
Best Local Similarity 89.3%; Pred. No. 2e-312;
Matches 1582; Conservative 0; Mismatches 0; Indels 190; Gaps 3;

1 CTGAGGCAACTTTGTTGACCATCTCCGCAATGCTTGGACGCTCTGATAGAGAGCTTT 60
2618 CTGAGGCAACTTTGTTGACCATCTCCGCAATGCTTGGACGCTCTGATAGAGAGCTTT 2671

61 TCCCTTAGTGTCCGAGAGTCTGCTCAACCTCTGAGGACTTCTTGAACCCCACTATCATGC 120
2672 -----AGGTGCCAGAGTCTGCTCAACCTCTGAGGACTTCTTGAACCCCACTATCATGC 2725

121 GGCAGGTGTTCTGCGAAACCCAGACAAGTCCAGTCCAGCAGGCA----- 168
2726 GGCAGGTGTTCTGCGAAACCCAGACAAGTCCAGTCCAGCAGGCGGTTTGTGTA 2785

169 ----- 168
2786 ACTGCGTTCTGACCTGCGGGAGAACTCCAGAGCTAGCAGGCTGAGGCTTCAGCC 2845

169 -----GAGCAGCATGCGCGAGCTGGTGGGTGAGCGGCTATGACAGCAGGAGG 218
2846 GAGCCTACCGGAGCAGCATGCGGAGCTGGTGGGTGAGCGGCTATGACAGCAGGAGG 2905

219 ACTTCTCTGTGTGTGAGCGCTTCTTCCAGAAATCCAGTCCCTGCTCTCTGGC----- 273
2906 ACTTCTCTGTGTGTGAGCGCTTCTTCCAGAAATCCAGTCCCTGCTCTCTGGC----- 2965

274 ----- 273
2966 GGTCTCCAGATAGTCTCTTCTTGTGCCCCAGACTGCATCCACCAATCAGAAATTCCTACT 3025

274 -----GCTTGAACCACTTGGAGCAAAACAGAGA 302
3026 CCCAGCTGGCAGAGCGCTTTGGACCAATATGCTTGAACCACTTGGAGCAAAACAGAGA 3085

303 CCCTGGACCTGAGAGCAGAGATGCCATCACTGTCTCCCACTCAGAAATGAGCCCTCTTGA 362
3086 CCCTGGACCTGAGAGCAGAGATGCCATCACTGTCTCCCACTCAGAAATGAGCCCTCTTGA 3145

363 GAACCCCTCGGAATAGTAATCACTACGTACCCATCAGCCAGCCATTTGAGAACTGGGGCA 422
3146 GAACCCCTCGGAATAGTAATCACTACGTACCCATCAGCCAGCCATTTGAGAACTGGGGCA 3205

XX PT Polynucleotides encoding human lipases that are structurally related to animal lipases, particularly phospholipase B, useful for drug screening, diagnosis and in gene therapy of biological disorders.

XX PT animal lipases, particularly phospholipase B, useful for drug screening, diagnosis and in gene therapy of biological disorders.

XX PS Claim 1; Page 36-37; 44pp; English.

XX XX The invention relates to a novel human lipase (NHL; ABB09555, ABB09556) and to nucleic acids encoding it (AB077623, AB077624). The NHL has structural similarity with animal lipases, particularly phospholipase B. Polynucleotides encoding NHL were obtained using human genomic sequences in conjunction with human thyroid and brain cDNAs. The NHL gene is located on chromosome 2, and contains a C/T polymorphism at position 3953 of the open reading frame (ORF), resulting in an Ala/Val substitution at position 1318 in the protein. NHL nucleotides and proteins are useful for treating disorders such as inflammatory or proliferative disease, infectious disease, clotting disorders, and cancer. They can also be used in screening for compounds useful in the treatment of mental, biological or medical disorders, as diagnostic reagents, in clinical trials monitoring and in cosmetic and nutritional applications. NHL nucleotides can additionally be used in the detection of disease-associated mutations, in the analysis of gene expression, for the recombinant expression of NHL, to generate transgenic animals, in gene therapy, and as part of ribozyme and/or triple helix sequences useful in the modulation of NHL gene expression. The present sequence represents the cDNA encoding the Ala 1318 variant of NHL.

XX XX Sequence 4377 BP; 1085 A; 1217 C; 1155 G; 920 T; 0 U; 0 Other;

XX SQ Query Match 74.2%; Score 1362; DB 6; Length 4377;
Best Local Similarity 89.3%; Pred. No. 2e-312;
Matches 1582; Conservative 0; Mismatches 0; Indels 190; Gaps 3;

QY 1 CTGAGGCAACTTTGTTGACCATCTCCGCAATGCTTGGACGCTCTGATAGAGAGCTTT 60
DB 2618 CTGAGGCAACTTTGTTGACCATCTCCGCAATGCTTGGACGCTCTGATAGAGAGCTTT 2671

QY 61 TCCCTTAGTGTCCGAGAGTCTGCTCAACCTCTGAGGACTTCTTGAACCCCACTATCATGC 120
DB 2672 -----AGGTGCCAGAGTCTGCTCAACCTCTGAGGACTTCTTGAACCCCACTATCATGC 2725

QY 121 GGCAGGTGTTCTGCGAAACCCAGACAAGTCCAGTCCAGCAGGCA----- 168
DB 2726 GGCAGGTGTTCTGCGAAACCCAGACAAGTCCAGTCCAGCAGGCGGTTTGTGTA 2785

QY 169 ----- 168
DB 2786 ACTGCGTTCTGACCTGCGGGAGAACTCCAGAGCTAGCAGGCTGAGGCTTCAGCC 2845

QY 169 -----GAGCAGCATGCGCGAGCTGGTGGGTGAGCGGCTATGACAGCAGGAGG 218
DB 2846 GAGCCTACCGGAGCAGCATGCGGAGCTGGTGGGTGAGCGGCTATGACAGCAGGAGG 2905

QY 219 ACTTCTCTGTGTGTGAGCGCTTCTTCCAGAAATCCAGTCCCTGCTCTCTGGC----- 273
DB 2906 ACTTCTCTGTGTGTGAGCGCTTCTTCCAGAAATCCAGTCCCTGCTCTCTGGC----- 2965

QY 274 ----- 273
DB 2966 GGTCTCCAGATAGTCTCTTCTTGTGCCCCAGACTGCATCCACCAATCAGAAATTCCTACT 3025

QY 274 -----GCTTGAACCACTTGGAGCAAAACAGAGA 302
DB 3026 CCCAGCTGGCAGAGCGCTTTGGACCAATATGCTTGAACCACTTGGAGCAAAACAGAGA 3085

QY 303 CCCTGGACCTGAGAGCAGAGATGCCATCACTGTCTCCCACTCAGAAATGAGCCCTCTTGA 362
DB 3086 CCCTGGACCTGAGAGCAGAGATGCCATCACTGTCTCCCACTCAGAAATGAGCCCTCTTGA 3145

QY 363 GAACCCCTCGGAATAGTAATCACTACGTACCCATCAGCCAGCCATTTGAGAACTGGGGCA 422
DB 3146 GAACCCCTCGGAATAGTAATCACTACGTACCCATCAGCCAGCCATTTGAGAACTGGGGCA 3205

1320 AACCAAGTGGCGCGAAGACTTACTCCAACTTACCCAGAGCGGAGCCAACTCAAGT 1379
4013 AACCAAGTGGCGCGAAGACTTACTCCAACTTACCCAGAGCGGAGCCAACTCAAGT 4072

1380 GCCCTCTCTGAGAGCCCTTACTCTACCTTACCCAGAGCGGAGCCAACTCAAGT 1439
4073 GCCCTCTCTGAGAGCCCTTACTCTACCTTACCCAGAGCGGAGCCAACTCAAGT 4132

1440 AGCTCAAGAGAGCCCGGAGGTGCTTACTTGGGCTGTCCAGTGGCAGCGGAGTCGGCC 1499
4133 AGCTCAAGAGAGCCCGGAGGTGCTTACTTGGGCTGTCCAGTGGCAGCGGAGTCGGCC 4192

1500 TTGTGTGGGCATCATCGGACAGTGGTCTGAGGTGAGGAGAGTGGCCGAGGGAAG 1559
4193 TTGTGTGGGCATCATCGGACAGTGGTCTGAGGTGAGGAGAGTGGCCGAGGGAAG 4252

1560 ATCTCCAAATGAGCTGCGCACTGTGGCCCTCTAGGCGCGGGGGTGGTCTCACCCCTAA 1619
4253 ATCTCCAAATGAGCTGCGCACTGTGGCCCTCTAGGCGCGGGGGTGGTCTCACCCCTAA 4312

1620 ACTCCCTATAGCACTCTTTCACCGCCCTCTGCGCCAGCCCTCCCGGCCACACGAGCA 1679
4313 ACTCCCTATAGCACTCTTTCACCGCCCTCTGCGCCAGCCCTCCCGGCCACACGAGCA 4372

1680 TGCTTCAATGCTGTGTCATAGGAGCCAGGAGCCAGGAGCACTTCTTTGG 1732
4373 TGCTTCAATGCTGTGTCATAGGAGCCAGGAGCCAGGAGCACTTCTTTGG 4425

RESULT 10
ABQ77623 standard; cDNA; 4377 BP.

AC ABQ77623;

21-OCT-2002 (first entry)

Human lipase NHL (Ala 1318 variant) cDNA.

Human; lipase; chromosome 2; phospholipase B homologue; thyroid; brain; inflammatory disease; proliferative disease; infectious disease; clotting disorder; cancer; drug screening; mental disorder; NHL; diagnostic reagent; clinical trial monitoring; cosmetic; nutraceutical; mutation detection; gene expression analysis; transgenic animal; neotrophic; cytostatic; antiinflammatory; single nucleotide polymorphism; SNP; gene therapy; gene; ss.

Homo sapiens.

Key Location/Qualifiers
CDS 1..4377
/*tag= a
/product= "Human lipase NHL"
replace(3953, T)
/*tag= b
/note= "Single nucleotide polymorphism (SNP); leads to an Ala to Val substitution at position 1318 of the protein"

variation

WO200259328-A1.
01-AUG-2002.
22-JAN-2002; 2002WO-US001715.
24-JAN-2001; 2001US-0264049P.
(LEXI-) LEXICON GENETICS INC.
Yu X, Miranda M, Turner CA;
WPI; 2002-599797/64.
P-PSDB; ABB09555.

QY 423 GTGACTTCCTGTGTACAGAGTGGGAAGGCTTCCAAATAGTGTTCCTCAACCTCTCTGTCCACCAGC 482
Db 3206 GTGACTTCCTGTGTACAGAGTGGGAAGGCTTCCAAATAGTGTTCCTCAACCTCTCTGTCCACCAGC 3265
QY 483 TCCGACACGACAGACATCAAAAGTGTGGCCGCCCTGGGTGACTCTCTGACTACACAGCTGG 542
Db 3266 TCCGACACGACAGACATCAAAAGTGTGGCCGCCCTGGGTGACTCTCTGACTACAGAGTGG 3325
QY 543 GAGCTCGACCAAAACAACTCCAGTACCTACCTACCAATCTTTGGAGGGGACTCTCTTTGGAGCA 602
Db 3326 GAGCTCGACCAAAACAACTCCAGTACCTACCAATCTTTGGAGGGGACTCTCTTTGGAGCA 3385
QY 603 TTGAGAGGGATGGGAACTTTGAGAGACTACACACACCTGCCCAACATTTCTGAAGAAGTTCA 662
Db 3386 TTGAGAGGGATGGGAACTTTGAGAGACTACACACACCTGCCCAACATTTCTGAAGAAGTTCA 3445
QY 663 ACCCTTACTCTCTGGCTTCTCTACCAAGCCTCGGAGGGGACAGCAGGACTTAATGTGG 722
Db 3446 ACCCTTACTCTCTGGCTTCTCTACCAAGCCTCGGAGGGGACAGCAGGACTTAATGTGG 3505
QY 723 CAGCGGAAGGGCCAGAGCTAGGACATGCCAGGCCCTGGGACCTGGGTAGAGCGAA 782
Db 3506 CAGCGGAAGGGCCAGAGCTAGGACATGCCAGGCCCTGGGACCTGGGTAGAGCGAA 3565
QY 783 TGA AAAA CAGCCCGACATCAACCTGGAGAAAGACTGGAAGCTGGTACACTTTCATTG 842
Db 3566 TGA AAAA CAGCCCGACATCAACCTGGAGAAAGACTGGAAGCTGGTACACTTTCATTG 3625
QY 843 GGGTCACAGACTCTGTCTACTTACTGTGAGATCCGAGGCCCACTTGGCCACGGAATATG 902
Db 3626 GGGTCACAGACTCTGTCTACTTACTGTGAGATCCGAGGCCCACTTGGCCACGGAATATG 3685
QY 903 TTCAAGCATCCAAAGCCCTCGACATCTCTCTGAGGAGCTCCCAAGGCTTTCTGTCA 962
Db 3686 TTCAAGCATCCAAAGCCCTCGACATCTCTCTGAGGAGCTCCCAAGGCTTTCTGTCA 3745
QY 963 ACCTGGTGGAGGTATGAGAGCTGGTACCTGTGTACAGGGCCAAAGGGGGAAATGTGCCA 1022
Db 3746 ACCTGGTGGAGGTATGAGAGCTGGTACCTGTGTACAGGGCCAAAGGGGGAAATGTGCCA 3805
QY 1023 TGCTGGCAGCTCAGAACCTGCACTTGCCTCAGACACTCGCAAGCTCCCTGGAGAGC 1082
Db 3806 TGCTGGCAGCTCAGAACCTGCACTTGCCTCAGACACTCGCAAGCTCCCTGGAGAGC 3865
QY 1083 AAGAACTGAAGAAAGTGAACCTGGAACCTCCAGCATGGCATCTCCAGTTTCTCTACTGGC 1142
Db 3866 AAGAACTGAAGAAAGTGAACCTGGAACCTCCAGCATGGCATCTCCAGTTTCTCTACTGGC 3925
QY 1143 ACCAATACACACAGGTGAGGACTTTTGGGTGTGGTGCAGCCTTTCTCCAAACACAC 1202
Db 3926 ACCAATACACACAGGTGAGGACTTTTGGGTGTGGTGCAGCCTTTCTCCAAACACAC 3985
QY 1203 TCACCCCACTGAACGAGAGGGGACACTGACCTCCTCTCTCTCCGAGGACTGTTTTT 1262
Db 3986 TCACCCCACTGAACGAGAGGGGACACTGACCTCCTCTCTCTCCGAGGACTGTTTTT 4045
QY 1263 ACTTCTCAGACCGGGGATGCCAGATGGCCATCGCACTCTGGAACAAACATGCTGCAAC 1322
Db 4046 ACTTCTCAGACCGGGGATGCCAGATGGCCATCGCACTCTGGAACAAACATGCTGCAAC 4105
QY 1323 CAGTGGGCGGCAAGACTACCTCCAACTTCAACCACTCCAGCGGACCAAACTCAAGTGCC 1382
Db 4106 CAGTGGGCGGCAAGACTACCTCCAACTTCAACCACTCCAGCGGACCAAACTCAAGTGCC 4165
QY 1383 CCTTCTCTGAGAGCCCTTACTCTACACCTTCGCGACAGCCGATGTCCTCCACACAGG 1442
Db 4166 CCTTCTCTGAGAGCCCTTACTCTACACCTTCGCGACAGCCGATGTCCTCCACACAGG 4225
QY 1443 CTGAAGAAGCCCGAGGTGCTCTACTTGGGTGTGTCAGTGGCAGCGGAGTGGCGCTTG 1502
Db 4226 CTGAAGAAGCCCGAGGTGCTCTACTTGGGTGTGTCAGTGGCAGCGGAGTGGCGCTTG 4285
QY 1503 TGGTGGGCATCATCGGACAGTGGTCTCTGGAGGTGCAGGAGGTGGCCGGAGGAAGATC 1562

Db 4286 TGGTGGGCATCATCGGACAGTGGTCTCTGGAGTGCAGGAGGTGGCCGGAGGAATC 4345
QY 1563 CTCCAATGAGCTCGCACCTGTGGCCCTCTAG 1594
Db 4346 CTCCAATGAGCTCGCACCTGTGGCCCTCTAG 4377
RESULT 11
ABQ77624
ID ABQ77624 standard; cDNA; 4377 BP.
XX AC ABQ77624;
XX DT 21-OCT-2002 (first entry)
XX Human lipase NHL (Val 1318 variant) cDNA.
XX Human; lipase; chromosome 2; phospholipase B homologue; thyroid; brain;
KW inflammatory disease; proliferative disease; infectious disease;
KW clotting disorder; cancer; drug screening; mental disorder; NHL;
KW diagnostic reagent; clinical trial monitoring; cosmetic; nutraceutical;
KW mutation detection; gene expression analysis; transgenic animal;
KW neotropic; cytostatic; antiinflammatory; single nucleotide polymorphism;
KW SNP; gene therapy; gene; ss.
XX OS Homo sapiens.
XX Key Location/Qualifiers
FT CDS 1..4377
FT /tag= a
FT /product= "Human lipase NHL"
FT variation replace(3953, C)
FT /tag= b
FT /note= "Single nucleotide polymorphism (SNP); leads to a
FT Val to Ala substitution at position 1318 of the protein"
XX WO200259328-A1.
XX 01-AUG-2002.
XX 22-JAN-2002; 2002WO-US001715.
XX 24-JAN-2001; 2001US-0264049P.
XX (LEXI-) LEXICON GENETICS INC.
XX Yu X, Miranda M, Turner CA;
XX WPI; 2002-599797/64.
XX P-PSDB; ABB09556.
XX Polynucleotides encoding human lipases that are structurally related to
XX animal lipases, particularly phospholipase B, useful for drug screening,
XX diagnosis and in gene therapy of biological disorders.
XX Disclosure; Page; 44pp; English.
XX The invention relates to a novel human lipase (NHL; ABB09555, ABB09556)
XX and to nucleic acids encoding it (ABQ77623, ABQ77624). The NHL has
XX structural similarity with animal lipases, particularly phospholipase B.
XX Polynucleotides encoding NHL were obtained using human genomic sequences
XX in conjunction with human thyroid and brain cDNAs. The NHL gene is
XX located on chromosome 2, and contains a C/T polymorphism at position 3953
XX of the open reading frame (ORF), resulting in an Ala/Val substitution at
XX position 1318 in the protein. NHL nucleotides and proteins are useful for
XX treating disorders such as inflammatory or proliferative disease,
XX infectious disease, clotting disorders, and cancer. They can also be used
XX in screening for compounds useful in the treatment of mental, biological
XX or medical disorders, as diagnostic reagents, in clinical trial
XX monitoring and in cosmetic and nutraceutical applications. NHL
XX associated mutations, in the analysis of gene expression, for the

CC recombinant expression of NHL, to generate transgenic animals, in gene
CC therapy, and as part of ribozyme and/or triple helix sequences useful in
CC the modulation of NHL gene expression. The present sequence represents
CC cDNA encoding the val 1318 variant of NHL. Note: The present sequence is
CC not shown in the specification, but was derived from the the information
CC given on page 18 and the Ala 1318 NHL-encoding cDNA (ABQ77623) given in
CC the sequence listing

XX Sequence 4377 BP; 1085 A; 1216 C; 1155 G; 921 T; 0 U; 0 Other;

SQ

Query Match 74.1%; Score 1360.4; DB 6; Length 4377;

Best Local Similarity 89.2%; Pred. No. 4.8e-312;

Matches 1581; Conservative 0; Mismatches 1; Indels 190; Gaps 3;

QY 1 CTGCAGCCAACTTTCTTGACCATCTCCGCAATGCTCTGGACGCTCTCGCATAGAGCCTTT 60

DB 2618 CTGCAGCCAACTTTCTTGACCATCTCCGCAATGCTCTGGACGCTCTCGCATAGAG 2671

QY 61 TCCTTTAGTGCACAGATCTCTGTCTCACTCTGGAATCTCTGAACCCCACTATCATCG 120

DB 2672 -----AGGTGCCAGAGCTCTGGTCAACCTCTGTGGACTTCTTGACCCCACTATCATCG 2725

QY 121 GGCAGGTGTTCTCTGGAAACCCAGACAAGTGCCTCAGTCAGCAGGCCA----- 168

DB 2726 GGCAGGTGTTCTCTGGAAACCCAGACAAGTGCCTCAGTCAGCAGGCCAAGTGTGTGTA 2785

QY 169 ----- 168

DB 2786 ACTGCGTTCTGACCTTCGCGGAGAACTCCCAAGAGCTAGCCAGCTGGAGCCTTCAGCC 2845

QY 169 -----GAGCAGCATGCGCGAGCTGCTGGGTGTCAGGCGGTATGACACGAGGAGG 218

DB 2846 GAGCCTACCGAGCAGCATGCGGAGCTGCTGGGTGTCAGGCGGTATGACACGAGGAGG 2905

QY 219 ACTTCTCTGTGGTGTGAGCCCTTCTTCAGAAATCCAGCTCCCTGCTCTGCGC----- 273

DB 2906 ACTTCTCTGTGGTGTGAGCCCTTCTTCAGAAATCCAGCTCCCTGCTCTGCGCGATG 2965

QY 274 ----- 273

DB 2966 GGCTCCCGATAGCTGCTCTTTTGCCCGAGCTGCATCCACCAATCAGAAATTCACACT 3025

QY 274 -----GCTTGAACCACTTCGAGCAAAACAGAGA 302

DB 3026 CCCAGCTGCCAGAGCCCTTTTGGACCAATATGTTGAACCATTTGGAGCAAAACAGAGA 3085

QY 303 CCCTGGACTCAGACGAGATGCCATCACTGTCCCACTCAGAAATGAGCCCTTCCTGA 362

DB 3086 CCCTGGACTCAGACGAGATGCCATCACTGTCCCACTCAGAAATGAGCCCTTCCTGA 3145

QY 363 GAAACCCCTCGGAATAGTAACTACAGTACCCCATCAAGCCAGCCATTGAGAACTGGGCA 422

DB 3146 GAAACCCCTCGGAATAGTAACTACAGTACCCCATCAAGCCAGCCATTGAGAACTGGGCA 3205

QY 423 GTGACTTCTGTGTACAGTGGAGGCTTCCAAATAGTGTTCCAAACCTCTGTCCACAGC 482

DB 3206 GTGACTTCTGTGTACAGTGGAGGCTTCCAAATAGTGTTCCAAACCTCTGTCCACAGC 3265

QY 483 TCCGACACGACACATCAAAGTGTGGCGCCCTGGGTGACTCTCTGACTACAGCAGTGG 542

DB 3266 TCCGACACGACACATCAAAGTGTGGCGCCCTGGGTGACTCTCTGACTACAGCAGTGG 3325

QY 543 GAGCTCGACCAACACTCCAGTGACCTTACCACATCTTGAGGGGACTCTCTTGAGACA 602

DB 3326 GAGCTCGACCAACAACTCCAGTGACCTTACCACATCTTGAGGGGACTCTCTTGAGACA 3385

QY 603 TTGAGGGGATGGGAATTTGGAGACTCAACCACTGCCCAAATTTCTGAGAGATTCA 662

DB 3386 TTGAGGGGATGGGAATTTGGAGACTCAACCACTGCCCAAATTTCTGAGAGATTCA 3445

QY 663 ACCCTTACCTCTTGGCTTCTGTACCAGACACTGGGAGGGGACAGCAGGACTTAATGTG 722

DB 3446 ACCCTTACCTCTTGGCTTCTGTACCAGACACTGGGAGGGGACAGCAGGACTTAATGTG 3505

cardiovascular disorder; central nervous system disorder; brain injury;
 chronic obstructive pulmonary disease; cerebrovascular disease; dementia;
 Alzheimer's disease; Parkinson's disease; corticobasal degeneration;
 motor neuron disease; Huntington's disease; Creutzfeldt Jacob dementia;
 schizophrenia; Korsakoff's psychosis; pain; epilepsy; multiple sclerosis;
 sciatica; stroke; age associated memory impairment; allergy; asthma;
 allergic rhinitis; hay fever; atopic dermatitis; cardiovascular disease;
 anaphylaxis; inflammation; acute respiratory distress syndrome; diabetes;
 chronic obstructive pulmonary disease; emphysema; obesity; anorexia;
 overweight; cachexia; bulimia; hypertension; coronary artery disease;
 type-II diabetes; hyperlipidaemia; gall bladder disease; osteoarthritis;
 gout; sleep apnoea; respiratory problem; polycystic ovarian syndrome;
 thrombolytic disease; reduced fertility; pregnancy; stress incontinence;
 hirsutism; menstrual irregularity; depression; enzyme; gene; ss.

Homo sapiens.

Key Location/Qualifiers
 CDS 1..3648
 /*tag= a
 /product= "Human phospholipase-like enzyme"
 /note= "CDS does not include start and stop codon"
 /partial

W0200231161-A2.

18-APR-2002.

09-OCT-2001; 2001WO-EP011641.

10-OCT-2000; 2000US-0238445P.

26-DEC-2000; 2000US-0257293P.

(FARB) BAYER AG.

Zhu Z;

WPI; 2002-426287/45.

P-PSDB; RAE22860.

New human phospholipase-like enzyme polypeptide useful for screening
 agents, and in the treatment of cancer, inflammation, diabetes, obesity,
 a central nervous system disorder, or a cardiovascular disorder.

Claim 19; Fig 1; 14app; English.

The present invention relates to novel human phospholipase-like enzymes
 and polynucleotides encoding such proteins. Sequences of the invention
 are useful for producing a medicament for modulating the activity of
 phospholipase in a disease such as cancer, inflammation, cardiovascular
 disorders, chronic obstructive pulmonary diseases, central nervous system
 (CNS) disorders such as brain injuries, cerebrovascular disease, dementia
 (Alzheimer's disease), Parkinson's disease, corticobasal degeneration,
 motor neuron disease, Pick's disease, Huntington's disease, Creutzfeldt
 Jacob dementia, schizophrenia with dementia, Korsakoff's psychosis, pain
 associated with CNS (e.g. epilepsy, stroke, age associated memory impairment,
 sciatica), multiple sclerosis, atopic allergic disease including asthma, allergic rhinitis (hay fever), atopic
 dermatitis, anaphylaxis and inflammation, cardiovascular disease, chronic
 obstructive pulmonary disease, acute respiratory distress syndrome, gout,
 diabetes, emphysema or obesity. They are also used for treating anorexia,
 overweight, cachexia, bulimia, hypertension, type-II diabetes, coronary
 artery disease, hyperlipidaemia, gall bladder disease, osteoarthritis,
 sleep apnoea and respiratory problems, cancer (e.g. breast, prostate,
 colon cancer), thrombolytic disease, reduced fertility, polycystic
 ovarian syndrome, complications of pregnancy, menstrual irregularity,
 hirsutism, stress incontinence and depression. The present sequence is
 human phospholipase like enzyme encoding cDNA

SQ Sequence 3648 BP; 899 A; 1032 C; 947 G; 770 T; 0 U; 0 Other;

Query Match 72.9%; Score 1337.2; DB 6; Length 3648;
 Best Local Similarity 88.8%; Pred. No. 1.4e-306;

Qy	1	CTGCAGCAAACTTTGTTGACCATCTCGCAATGCTTTGGAGCTCTGTCATAGAGAGCTTT	60
Db	1901	CTGCAGCAAACTTTGTTGACCATCTCGCAATGCTTTGGAGCTCTGTCATAGAGAGCTTT	1954
Qy	61	TCCTTTAGTGGCCAGAGTCTCTGTTCAACTCTGTTGAGTCTCTTGAACCCCACTATCATGC	120
Db	1955	-----AGTGGCCAGAGTCTCTGTTCAACTCTGTTGAGTCTCTTGAACCCCACTATCATGC	2008
Qy	121	GGCAGGTGTTCTCTGGGAAACCCAGACAAGTGGCCAGTGCAGCAGGCCA-----	168
Db	2009	GGCAGGTGTTCTCTGGGAAACCCAGACAAGTGGCCAGTGCAGCAGGCCA-----	2068
Qy	169	-----	168
Db	2069	ACTGCGTTCTGACCTCGGGGAGNACTCCCAAGAGTAGCCAGGCTGGAGGCTTCAGCC	2128
Qy	169	-----GAGCAGCATGCGGAGTGTGGGGTCAAGCCGCTATGACACGAGGAGG	218
Db	2129	GAGCCTACCGGAGCAGCATGCGGAGTGTGGGGTCAAGCCGCTATGACACGAGGAGG	2188
Qy	219	ACTTCTCTGTGTGCTGCAGCCCTTCTTCCAGAACATCCAGCTCCCTGCTCTGGC-----	273
Db	2189	ACTTCTCTGTGTGCTGCAGCCCTTCTTCCAGAACATCCAGCTCCCTGCTCTGGC-----	2248
Qy	274	-----	273
Db	2249	GGCTCCAGATACGTCTCTTTGCCCCAGAGTCATCCACCACCAATTCAGAAATTCACCT	2308
Qy	274	-----GCTTGAACCACTTTGGAAGCAAAACAGAGA	302
Db	2309	CCAGCTGGCCAGAGCCCTTTGGACCAATATGCTTGAACCACTTTGGAAGCAAAACAGAGA	2368
Qy	303	CCCTGGACCTGAGAGCAGAGATGCCCCATCACTGTCCCATCAGAAATGAGCCCTTCTGA	362
Db	2369	CCCTGGACCTGAGAGCAGAGATGCCCCATCACTGTCCCATCAGAAATGAGCCCTTCTGA	2428
Qy	363	GAACCCCTCGGAATAGTAACCTACACGTACCCCATCAAGCCAGCCATTTGAGAACTGGGGCA	422
Db	2429	GAACCCCTCGGAATAGTAACCTACACGTACCCCATCAAGCCAGCCATTTGAGAACTGGGGCA	2488
Qy	423	GTGACTTCTGTGTACAGAGTGAAGGCTTCCAAATAGTGTTCACCACTCTGTCCACGAGC	482
Db	2489	GTGACTTCTGTGTACAGAGTGAAGGCTTCCAAATAGTGTTCACCACTCTGTCCACGAGC	2548
Qy	483	TCGACCCAGCAGATCAAAAGTGGTGGCCGCTCTGGTGGTACTCTCTGACTACAGCACTGG	542
Db	2549	TCGACCCAGCAGATCAAAAGTGGTGGCCGCTCTGGTGGTACTCTCTGACTACAGCACTGG	2608
Qy	543	GAGCTCGACCAAACTCTCCAGTGACCTACCCACATCTTGGAGGGGACTCTCTTGGAGCA	602
Db	2609	GAGCTCGACCAAACTCTCCAGTGACCTACCCACATCTTGGAGGGGACTCTCTTGGAGCA	2668
Qy	603	TTGGAGGGGATGGAACTTTGGAGACTCACACCACTGCCCCAACATTTCTGAAGAAGTTCA	662
Db	2669	TTGGAGGGGATGGAACTTTGGAGACTCACACCACTGCCCCAACATTTCTGAAGAAGTTCA	2728
Qy	663	ACCTTACCTCTCTGGTCTTCTTACAGCACTTGGAGGGGAGCAGCAGGACTAAATGTTG	722
Db	2729	ACCTTACCTCTCTGGTCTTCTTACAGCACTTGGAGGGGAGCAGCAGGACTAAATGTTG	2788
Qy	723	CAGCGAAGGGGCGAGAGCTAGGAGCATGCGACCCAGGCTCTGGAGCTCTGGTAGAGCGAA	782
Db	2789	CAGCGAAGGGGCGAGAGCTAGGAGCATGCGACCCAGGCTCTGGAGCTCTGGTAGAGCGAA	2848
Qy	783	TGAAAAACAGCCCCGACATCAACTCTGGAGAAAGACTGGAAAGCTGGTCACTCTTCAATTG	842
Db	2849	TGAAAAACAGCCCCGACATCAACTCTGGAGAAAGACTGGAAAGCTGGTCACTCTTCAATTG	2908
Qy	843	GGGTCAACGACTTGTGTCTATTACTGTGAGAAATCGGAGGGCCCACTTGGCCACGGAATATG	902
Db	2909	GGGTCAACGACTTGTGTCTATTACTGTGAGAAATCGGAGGGCCCACTTGGCCACGGAATATG	2968

DR P-PSDB; ABU65081.
XX NOXV polypeptides and polynucleotides, useful for preventing or treating
PT a disorder associated with aberrant NOXV expression or activity e.g.,
PT cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
PT asthma.
XX
PS Claim 13; Page 167-168; 1103pp; English.
XX
CC This invention describes novel human NOXV polypeptides which have
CC cytosolic, cardiac, antiarteriosclerotic, antiasthmatic and hypotensive
CC activity. Pharmaceutical compositions comprising the NOXV proteins or
CC nucleic acid molecules or NOXV antibodies are useful for preventing or
CC treating a disorder associated with aberrant NOXV expression or activity
CC e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
CC asthma. The products of the invention can be used for gene therapy or in
CC a vaccine. ABX97008-ABX97185 are cDNA fragments amplified and isolated by
CC the PCR primers and probes represented in ABX13460-ABX13462 and ABX97186-
CC ABX97593. ABX97008-ABX97185 encode the NOXV proteins described in
CC ABU65041-ABU65218
XX
SQ Sequence 4268 BP; 1039 A; 1209 C; 1119 G; 901 T; 0 U; 0 Other;
Query Match 67.1%; Score 1231.8; DB 6; Length 4268;
Best Local Similarity 86.1%; Pred. No. 1.5e-281;
Matches 1535; Conservative 0; Mismatches 37; Indels 211; Gaps 7;
1 CTGCAGCCAACTTTGTTGACCATCTCCGCAATGCTTGGAGCTCTGCATAGAGAGCTTT 60
2516 CTGCAGCCAACTTTGTTGACCATCTCCGCAATGCTTGGAGCTCTGCATAGAG- 2569
61 TCCCTTAGTGCCAGAGTCTGTGCAACTCTGTGGACTTCTTGAACCCCACTATATGC 120
2570 -----AGGTGCCAGAGTCTGTGTCAACTCTGTGGACTTCTTGAACCCCACTATATGC 2623
121 GGCAGGTGTTCTTGGAAACCCAGACAGTGTCCAGTCCAGTCCAGCAGG- 165
2624 GGCAGGTGTTCTTGGAAACCCAGACAGTGTCCAGTCCAGTCCAGCAGGCGTTTGTGTA 2683
166 ----- 165
2684 ACTGGTCTGACCTTGGGGAGAACTCCCAAGAGTAGCCAGGCTGGAGGCTTCAGCC 2743
166 -----CCAGAGCAGATGCGAGCTGTGGGTGAGCCGCTATGACACGAGGAGG 218
2744 GAGCCTACACAGCAGCATGCGGAGCTGTGGGTGAGGCGCTATGACACGAGGAGG 2803
219 ACTTCTGTGGTGTGAGCCCTTCTTCCAGACATCCAGTCCCTGTCTG- 271
2804 ACTTCTGTGGTGTGAGCCCTTCTTCCAGACATCCAGTCCCTGTCTGAGGATG 2863
272 ----- 271
2864 GGCTCCAGATACGTCCTTCTTTGCCCGAGACTGCATCCACCAGAAATCCAGT 2923
272 -----GGCTTGAACCACTTTGGAAGCAAAACAGAGA 302
2924 CCCAGCTGGCCAGAGCCCTTTGGACCAATATGCTTGAACCACTTTGGAAGCAAAACAGAGA 2983
303 CCCTGGACCTGAGACAGAGATGCCATCAGTCTCCCACTCAGAAATGAGCCCTTCTGA 362
2984 CCCTGGACCTGAGACAGAGATGCCATCAGTCTCCCACTCAGAAATGAGCCCTTCTGA 3043
363 GAACCCCTCGGAATAGTAAGTACAGTACACGTTACCCATCAAGCCAGGCAATGGGGCA 422
3044 GAACCCCTCGGAATAGTAAGTACAGTACACGTTACCCATCAAGCCAGGCAATGGGGCA 3103
423 GTGACTTCTGTGACAGAGTGAAGGCTTCCAAATAGTGTTCAAACCTCTGTCCACCAGC 482
3104 GTGACTTCTGTGACAGAGTGAAGGCTTCCAAATAGTGTTCAAACCTCTGTCCACCAGC 3163
483 TCCGACACAGACATCAAGTGTGGCGCCCTTGGGTGACTCTCTGACTACAGAGTGG 542

Db 3164 TCCGACACGACGACATCAAAAGTGGTGGCGCCCTTGGGTGACTCTCTGACTACAGCAGTGG 3223
Qy 543 GAGCTCGACCAAAACAACTCCAGTACCTACCCACATCTTGGAGGGGACTCTCTTGGAGCA 602
Db 3224 GAGCTCGACCAAAACAACTCCAGTACCTACCCACATCTTGGAGGGGACTCTCTTGGAGCA 3283
Qy 603 TTGAGGGGATGGGAACTTTGGAGACTCACACACACTTGCACCAATTTCTGAAGAAGTTCA 662
Db 3284 TTGAGGGGATGGGAACTTTGGAGACTCACACACACTTGCACCAATTTCTGAAGAAGTTCA 3343
Qy 663 ACCCTTACCTCTCTGGCTTCTTACACAGCACTTGGAGGGGACAGCAGGACTTAATATGG 722
Db 3344 ACCCTTACCTCTCTGGCTTCTTACACAGCACTTGGAGGGGACAGCAGGACTTAATATGG 3403
Qy 723 CAGCGGAAGGGGCGCAGAGCT---AGGACATGCCAGCCAGGCTTGGAGCCCTGTAGAGC 779
Db 3404 CAGCGGAAGGGGCGCAGAGCTAGGAGGGACATGCCAGCCAGGCTTGGAGCCCTGTAGAGC 3463
Qy 780 GAATGAAAAACAGCCCGACATCAACCTGGAGAAAGACTGGAGCTGGTCACTCTTCA 839
Db 3464 GAATGAAAAACAGCCC---CATACACTTTCAGGAAGACTTGAAGATAATAACCCCTGT 3520
Qy 840 TTGGGGTCAACGACTTGTCTTACTTGTGAGTCCGAGGATCCGAGGCCACTTGGCCACGAAT 899
Db 3521 TAGCGGCAATGACTCTGTGATTTCTGCAATGATC-----TGTAGTGAAT 3568
Qy 900 ATGTTACGACATCCAAACAGGCCCTTGACATCTCTCTGAGGAGCTCCCAAGGGCTTTTCG 959
Db 3569 ATGTTACGACATCCAAACAGGCCCTTGACATCTCTCTGAGGAGCTCCCAAGGGCTTTTCG 3628
Qy 960 TCAACGTGTGGAGGTTCATGAGCTGTGCTGATACGCTGTACAGGGCAAGGGGGGAAATGTG 1019
Db 3629 TCAACGTGTGGAGGTTCATGAGCTGTGCTGATACGCTGTACAGGGCAAGGGGGGAAATGTG 3688
Qy 1020 CCATGTGGCAGCTCAAGCAAACTGCACTTGGCTCAGACACTCGCAAGCTCCCTGGAGA 1079
Db 3689 CCATGTGGCAGCTCAAGCAAACTGCACTTGGCTCAGACACTCGCAAGCTCCCTGGAGA 3748
Qy 1080 AGCAAGAACTGAAAGAAAGTGAACCTTGGAACTCCAGCATGGCATCTCCAGTTTCTCTACT 1139
Db 3749 AGCAAGAACTGAAAGAAAGTGAACCTTGGAACTCCAGCATGGCATCTCCAGTTTCTCTACT 3808
Qy 1140 GGCAACCAATACACACGCTGAGGACTTTTGGGTGTGGTGTGAGCCCTTTTCCAAACA 1199
Db 3809 GGCACCAATACACACGCTGAGGACTTTGCGGTGTGGTGTGAGCCCTTTTCCAAACA 3868
Qy 1200 CACTCACCCCACTGAACGAGAGGGGACACTGACCTCAGCTTCTTCCGAGGACTGTT 1259
Db 3869 CACTCACCCCACTGAAC---AGAGGGGACACTGACCTCAGCTTCTTCCGAGGACTGTT 3925
Qy 1260 TTCACTTCTCAGACCGCGGCATGCCAGATGGCCATCGCACTCTGGAAACAACTGCTGG 1319
Db 3926 TTCACTTCTCAGACCGCGGCATGCCAGATGGCCATCGCACTCTGGAAACAACTGCTGG 3985
Qy 1320 AACAGTGGCGGCAAGACTTACTTCCAACTTCAACCACTTCCAGCCAGCCGAGCCAACTCAAGT 1379
Db 3986 AACAGTGGCGGCAAGACTTACTTCCAACTTCCAACTTCCAGCCAGCCGAGCCAACTCAAGT 4045
Qy 1380 GCCCTCTCTGAGAGCCCTTACTCTACACCTTCCGGAACAGCCGATGCTCTCCAGACC 1439
Db 4046 GCCCTCTCTGAGAGCTTACTCTACACCTTCCGGAACAGCCGATGCTCTCCAGACC 4105
Qy 1440 AGGTGAAGAAGCCCGAGGTGCTTACTTGGGTGTGCTCCAGTGGCAGCGGAGTCTGGCC 1499
Db 4106 AGGTGAAGAAGCCCGAGGTGCTTACTTGGGTGTGCTCCAGTGGCAGCGGAGTCTGGCC 4165
Qy 1500 TTGTGTGGGCAATCATCGGACAGTGTCTGTGGAGTTCAGAGAGTGGCGGAGGGAAG 1559
Db 4166 TTGTGTGGGCAATCATCGGACAGTGTCTGTGGAGTTCAGAGAGTGGCGGAGGGAAG 4225
Qy 1560 ATCTTCAATGAGCCTGGCAGCTGTGGCCCTCTAGGCCCGGGG 1602
Db 4226 ATCTTCAATGAGCCTGGCAGCTGTGGCCCTCTAGGCCCGGGG 4268

Db	3809	GGCACC	AAATACACACAGCGT	GAGCACTTTTGGGGTTGTGGTGAGACCTTTCTTCCAAAACA	3868
Qy	1200	CAC	TCA	CCCCCACTGAACAGAGAGAGGGGACACTGACCTTCACTCTTCTCCGAGGACTGTT	1259
Db	3869	CAC	TCA	CCCCCACTGAACTGAGCTTCTCCGAGGACTGTT	3925
Qy	1260	TTCACT	TTCTCAGACCGCGGGCATGCGAGATGGCGATCGCACTCTGGAAACAACATGCTGG	1319	
Db	3926	TTCACT	TTCTCAGACCGCGGGCATGCGAGATGGCGATCGCACTCTGGAAACAACATGCTGG	3985	
Qy	1320	AAC	CAGTGGGCGCCAGACCTACCTCCAAACAATTCACCCACAGCGGAGCCAAACTCAAGT	1379	
Db	3986	AAC	CAGTGGGCGCCAGACCTACCTCCAAACAATTCACCCACAGCGGAGCCAAACTCAAGT	4045	
Qy	1380	GC	CCCTCTCTGAGAGCCCTTACCTCTACACCTCTGCGGAACAGCCGATTTGCTCCAGACC	1439	
Db	4046	GC	CCCTCTCTGAGTCCCTTACCTCTACACCTCTGCGGAACAGCCGATTTGCTCCAGACC	4105	
Qy	1440	AGG	CTGAAGAAGCCCGGAGGTGCTTACTCTGGGGTGTCTCCAGTGGCAAGCGGAGTCTGGCC	1499	
Db	4106	AGG	CTGAAGAAGCCCGGAGGTGCTTACTCTGGGGTGTCTCCAGTGGCAAGCGGAGTCTGGCC	4165	
Qy	1500	TTCT	GTGTGGGCATCATCGGACAGTGGTCTCTGGAGGTGCACGAGAGGTGGCCGGAGGGAAG	1559	
Db	4166	TTGT	GTGTGGGCATCATCGGACAGTGGTCTCTGGAGGTGCACGAGAGGTGGCCGGAGGGAAG	4225	
Qy	1560	AT	CTCTCAATGAGCTGCGCACTGTGGCCCTCTAGGCCCGGGG	1602	
Db	4226	AT	CTCTCAATGAGCTGCGCACTGTGGCCCTCTAGGCCCGGGG	4268	
RESULT 15					
ADN61812					
ID ADN61812 standard; cDNA; 4268 BP.					
AC	ADN61812;				
XX	01-JUL-2004 (first entry)				
XX	Human cDNA encoding NOV24a.				
DE	Human; ss; gene; NOVX; diabetes; obesity; infectious disease; anorexia;				
KW	cancer-associated cachexia; cancer; neurodegenerative disorder;				
KW	Alzheimer's disease; Parkinson's disease; immune disorder;				
KW	haematopoietic disorder; dyslipidaemia; chronic disease.				
OS	Homo sapiens.				
XX	US2004043382-A1.				
XX	04-MAR-2004.				
XX	07-MAR-2002; 2002US-00092900.				
XX	08-MAR-2001; 2001US-0274191P.				
PR	08-MAR-2001; 2001US-0274194P.				
PR	08-MAR-2001; 2001US-0274281P.				
PR	08-MAR-2001; 2001US-0274322P.				
PR	09-MAR-2001; 2001US-0274849P.				
PR	12-MAR-2001; 2001US-0275235P.				
PR	13-MAR-2001; 2001US-0275578P.				
PR	13-MAR-2001; 2001US-0275579P.				
PR	14-MAR-2001; 2001US-0275601P.				
PR	16-MAR-2001; 2001US-0276000P.				
PR	16-MAR-2001; 2001US-0276776P.				
PR	19-MAR-2001; 2001US-0276994P.				
PR	20-MAR-2001; 2001US-0277239P.				
PR	20-MAR-2001; 2001US-0277321P.				
PR	20-MAR-2001; 2001US-0277327P.				
PR	20-MAR-2001; 2001US-0277338P.				
PR	21-MAR-2001; 2001US-0277791P.				
PR	22-MAR-2001; 2001US-0277833P.				
PR	23-MAR-2001; 2001US-0278152P.				

PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
XX Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L;
PI Zernhusen BD, Gusev VV, Ji W, Gorman L, Miller CE, Kekuda R;
PI Patturajan M, Gangolli EA, Vernet CAM, Guo XS, Tchernev VT;
PI Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y;
PI Anderson JW, Spaderna SK, Catterton E, Leite MW, Zhong H;
PI Alsobrook JP, Lepley DW, Rieger DK, Burgess CE,
XX WPI: 2004-225693/21.
DR P-PSDB; ADN61813.
DR
XX New NOVX polypeptides and nucleic acid molecules useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. cancer, diabetes,
PT infection or obesity, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
PT
XX Claim 17; SEQ ID NO 81; 786pp; English.
PS
XX The invention relates to an isolated polypeptide (designated NOVX, or
CC NOV1-NOV127) comprising a sequence selected from 178 fully defined amino
CC acid sequences (and their mature forms, variants and fragments). Also
CC included are an isolated nucleic acid molecule encoding NOVX, a vector
CC comprising the nucleic acid, a cell comprising the vector, methods for
CC determining the presence or amount of the polypeptide or the nucleic acid
CC molecule in a sample, methods for determining the presence of or
CC predisposition to a disease associated with altered levels of expression
CC of the above polypeptide or nucleic acid molecule in a first mammalian
CC subject, a method for identifying an agent that binds to the above
CC polypeptide, a method for identifying a potential therapeutic agent for
CC use in the treatment of a pathology that is related to aberrant
CC expression or physiological interactions of the polypeptide, a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide and a method for modulating
CC the activity of the polypeptide cited above. The composition and methods
CC are useful for diagnosing, preventing or treating diseases such as
CC diabetes, obesity, infectious diseases, anorexia, cancer-associated
CC cachexia, cancer, neurodegenerative disorders like Alzheimer's disease or
CC Parkinson's disease, immune disorders, haematopoietic disorders,
CC dyslipidaemias, and other chronic diseases. These may also be used in
CC chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The polypeptides are also useful as vaccines. The
CC present sequence encodes a NOVX protein of the invention.
XX
SQ Sequence 4268 BP; 1039 A; 1214 C; 1114 G; 901 T; 0 U; 0 Other;
Query Match 67.0%; Score 1230.2; DB 12; Length 4268;
Best Local Similarity 86.0%; Pred. No. 3.6e-281; Indels 211; Gaps 7;
Matches 1534; Conservative 0; Mismatches 38;
QY 1 CTGCAGCCAACTTTGTTGACCATCTCCGAATGCTTGGAGCTCTGATAGAGAGCTTT 60
Db 2516 CTGCAGCCAACTTTGTTGACCATCTCCGAATGCTTGGAGCTCTGATAGAGAGCTTT 2569
QY 61 TCCCTTTAGTGGCCAGAGTCTTGTCACCTCTGTCGACTTCTGAACCCCACTATATGC 120
Db 2570 -----AGTGGCCAGAGTCTTGTCACCTCTGTCGACTTCTGAACCCCACTATATGC 2623
QY 121 GGCAGGTGTTCTGGGAAACCCAGACAGTCCCAAGTGCAGCAGG----- 165
Db 2624 GGCAGGTGTTCTGGGAAACCCAGACAGTCCCAAGTGCAGCAGGCGTTTGTGTGTA 2683
QY 166 ----- 165
Db 2684 ACTGCGTTCTGACCTTCGCGGAGAACTCCCAAGAGTACCGAGGTGGAGGCTTCAGCC 2743
QY 166 -----CCAGAGCAGCATCGCGAGCTGGTGGGGTCAGCGCGCTATGACAGCAGGAGG 218
Db 2744 GAGCCTACAGCAGCAGCATGCGGAGCTGTGGGGTCAGCGCGCTATGACAGCAGGAGG 2803
QY 219 ACTTCTCTGTGTGCTGTGACGCCCTTCTTCCAGAACATCCAGCTCCCTGTCCTG----- 271
PA (PADI/) PADIGARU M.
PA (SPYT/) SPYTEK K A.
PA (SHEN/) SHENOY S G.
PA (TAUP/) TAUPIER R J.
PA (PENA/) PENNA C E A.
PA (LILL/) LI L.
PA (ZERN/) ZERNHUSEN B D.
PA (GUSE/) GUSEV V Y.
PA (JIWW/) JI W.
PA (GORM/) GORMAN L.
PA (MILL/) MILLER C E.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTURAJAN M.
PA (GANG/) GANGOLLI E A.
PA (VERN/) VERNET C A M.
PA (GUOX/) GUO X S.
PA (TCHE/) TCHERNEV V T.
PA (FERN/) FERNANDES E R.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (GERL/) GERLACH V.
PA (LIUY/) LIU Y.
PA (ANDE/) ANDERSON D W.
PA (SPAD/) SPADERNA S K.
PA (CATT/) CATTERTON E.
PA (LEIT/) LEITE M W.
PA (ZHON/) ZHONG H.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.

Db 2804 ACTTCTGTGTGTGTCAGAGCCCTTCTTCCAGAAATCCAGCTCCCTGTCTGTGAGGATG 2863
Qy 272 ----- 271
Db 2864 GGCTCCAGATACGTCCTTCTTTGGCCCGAGACTGCATCCACCAATCAGAAATTCACACT 2923
Qy 272 ----- GGCCTTGAAACCACTTTGGAAGCAAAACAGAGA 302
Db 2924 CCCAGCTGGCCAGACCCCTTTTGGACCAATATGCTTTGAACCACTTTGGAAGCAAAACAGAGA 2983
Qy 303 CCCTGGACCTGAGAGCAGAGATGCCATCAGCTGTCCCACTCAGAAATGAGCCCTTCCTGA 362
Db 2984 CCCTGGACCTGAGAGCAGAGATGCCATCAGCTGTCCCACTCAGAAATGAGCCCTTCCTGA 3043
Qy 363 GAAACCCCTCGGAATAGTAACCTACAGTACCCCACTCAAGCCAGCCATTGAGAACTGGGGCA 422
Db 3044 GAAACCCCTCGGAATAGTAACCTACAGTACCCCACTCAAGCCAGCCATTGAGAACTGGGGCA 3103
Qy 423 GTGACTTCTGTGTACAGAGTGGAAAGCTTCCAAATAGTGTTCACACCTCTCTCCACGAGC 482
Db 3104 GTGACTTCTGTGTACAGAGTGGAAAGCTTCCAAATAGTGTTCACACCTCTCTCCACGAGC 3163
Qy 483 TCCGACACGACAGATCAAAAGTGTGGCCGCTGGGTGACTCTCTGACTACAGCAGTGG 542
Db 3164 TCCGACACGACAGATCAAAAGTGTGGCCGCTGGGTGACTCTCTGACTACAGCAGTGG 3223
Qy 543 GAGCTCGACCAACAACTCCAGTGAACCTTACCCACATCTTGGAGGGAGCTCTTTGGAGCA 602
Db 3224 GAGCTCGACCAACAACTCCAGTGAACCTTACCCACATCTTGGAGGGAGCTCTTTGGAGCA 3283
Qy 603 TTGAGGGGATGGGAACCTTGGAGACTCACACCACTGCCCCAAATTTCTGAAGAAAGTTCA 662
Db 3284 TTGAGGGGATGGGAACCTTGGAGACTCACACCACTGCCCCAAATTTCTGAAGAAAGTTCA 3343
Qy 663 ACCCTTACTCTCTTGGCTTCTTCTACAGCAGCTGGAGGGGACAGCAGGACTAATGTGG 722
Db 3344 ACCCTTACTCTCTTGGCTTCTTCTACAGCAGCTGGAGGGGACAGCAGGACTAATGTGG 3403
Qy 723 CAGCGGAAGGGCCAGAGCT---AGGGACATGCCAGGCCAGGCCCTGGGACCTGGTAGAGC 779
Db 3404 CAGCGGAAGGGCCAGAGCTAGGAGGGACATGCCAGGCCAGGCCCTGGGACCTGGTAGAGC 3463
Qy 780 GAATGAAACACAGCCCGACATCAACCTGGAGAAAGACTGGAAGCTGGTCAACCTCTTCA 839
Db 3464 GAATGAAACACAGCC---CATACACTTTCAGGAAGACTGGAAGATAATAACCTCTGTTA 3520
Qy 840 TTGGGGTCAACGACTTGTGTCAATTACTGTGAGATCCGGAGGCCCACTTGGCCACGGAT 899
Db 3521 TAGCGGGCAATGACCTCTGTGATTTCTGCAATGATC-----TGGTAGGTGAAT 3568
Qy 900 ATGTTACGACATGCCAACAGGCCCTGGACATCCTCTCTGAGGAGCTCCCAAGGGCTTTTCG 959
Db 3569 ATGTTACGACATGCCAACAGGCCCTGGACATCCTCTCTGAGGAGCTCCCAAGGGCTTTTCG 3628
Qy 960 TCAACGTGTGGAGGTCAATGAGCTGGCTAGCCTGTATCCAGGGCCAAAGGGGGAAATGTG 1019
Db 3629 TCAACGTGTGGAGGTCAATGAGCTGGCTAGCCTGTATCCAGGGCCAAAGGGGGAAATGTG 3688
Qy 1020 CCATGCTGGAGCTCAGAACAACTGCACTTGCCTCAGACACTCGCAAGCTCCCTGGAGA 1079
Db 3689 CCATGCTGGAGCTCAGAACAACTGCACTTGCCTCAGACACTCGCAAGCTCCCTGGAGA 3748
Qy 1080 AGCAAGAACTGAAGAAAGTGAACCTGGAACTCCAGCATGGCATCTCCAGTTTCTCTCTACT 1139
Db 3749 AGCAAGAACTGAAGAAAGTGAACCTGGAACTCCAGCATGGCATCTCCAGTTTCTCTCTACT 3808
Qy 1140 GGCAACCAATACACAGCGTGAGGACTTTGCGGTGTGTGGTGACGCTTTCTTCCAAAACA 1199
Db 3809 GGCAACCAATACACAGCGTGAGGACTTTGCGGTGTGTGGTGACGCTTTCTTCCAAAACA 3868
Qy 1200 CACTCAGCCCACTGAACGAGAGAGGGGACACTGACCTTCTTCTCCGAGGACTGTT 1259
Db 3869 CACTCAGCCCACTGAAC---AGAGGGGACACTGACCTCACCTTCTTCTCCGAGGACTGTT 3925

Qy 1260 TTCACTTCTCAGACCGGGGGCATGCCGAGATGGCCATCGCACTCTTGGAAACAAACATGCTGG 1319
Db 3926 TTCACTTCTCAGACCGGGGGCATGCCGAGATGGCCATCGCACTCTTGGAAACAAACATGCTGG 3985
Qy 1320 AACCAAGTGGGCGCAAGACTTACCTTCCAACTTCAACCAAGCCAGCGGAGCCAACTCAAAGT 1379
Db 3986 AACCAAGTGGGCGCAAGACTTACCTTCCAACTTCAACCAAGCCAGCGGAGCCAACTCAAAGT 4045
Qy 1380 GCGCCTCTCTCAGAGAGCCCTTACCTCTACACCTTGGGAAACAGCCGATTGCTCCAGACC 1439
Db 4046 GCGCCTCTCTCAGAGAGCCCTTACCTCTACACCTTGGGAAACAGCCGATTGCTCCAGACC 4105
Qy 1440 AGGCTGAAGAAAGCCCGAGGTGCTTACTGGGCTGTCCCAAGTGGCAGCGGGAGTCCGCC 1499
Db 4106 AGGCTGAAGAAAGCCCGAGGTGCTTACTGGGCTGTCCCAAGTGGCAGCGGGAGTCCGCC 4165
Qy 1500 TTGTGGTGGGATCATCGGGACAGTGTCTTGGAGGTGAGAGAGGTGGCCGAGGGAG 1559
Db 4166 TTGTGGTGGGATCATCGGGACAGTGTCTTGGAGGTGAGAGAGGTGGCCGAGGGAG 4225
Qy 1560 ATCCTCCAATGAGCCTGGCAGCTGTGGCCCTCTTAGGCCCGGGG 1602
Db 4226 ATCCTCCAATGAGCCTGGCAGCTGTGGCCCTCTTAGGCCCGGGG 4268

Search completed: March 26, 2005, 14:31:15
Job time : 982.6 secs

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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 13:16:45 ; Search time 322.751 Seconds
(without alignments)
9303.061 Million cell updates/sec

Title: US-09-778-961-1
Perfect score: 1835
Sequence: 1 ctgcagccaactttgttgac.....aaaaaaaaaaaaaaaaaaaaa 1835

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405588

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA.*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
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5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	135.2	7.4	373	4	US-09-471-276-571
2	107.2	5.8	645	4	US-09-270-767-12725
3	62.2	3.4	323	4	US-09-270-767-28539
4	49.6	2.7	6065	4	US-09-800-729-35
5	49.4	2.7	193	4	US-09-621-976-10543
6	48.2	2.6	1141	4	US-09-800-729-78
7	48.2	2.6	1937	4	US-09-647-143-1
8	48.2	2.6	2329	4	US-09-800-729-11
9	48.2	2.6	2355	4	US-09-800-729-27
10	47.6	2.6	1976	4	US-09-920-759-10
11	47.2	2.6	2065	3	US-09-370-473-5
12	47.2	2.6	4494	4	US-09-620-312D-861
13	47	2.6	630	4	US-09-621-976-12892
14	47	2.6	601	4	US-09-949-016-161396
15	47	2.6	688	6	5498694-3
16	47	2.6	688	6	5498694-3
17	47	2.6	882	4	US-09-311-021-107
18	47	2.6	240157	4	US-09-949-016-16264
19	46.8	2.6	173	4	US-09-621-976-9851
20	46.8	2.6	272	4	US-09-270-767-11902
21	46.8	2.6	358	4	US-09-621-976-927
22	46.8	2.6	711	4	US-09-621-976-17854
23	46.8	2.6	1493	1	US-08-340-820-24
24	46.8	2.6	1493	1	US-08-593-535-24
25	46.8	2.6	82268	4	US-09-949-016-14178
26	46.6	2.5	2083	4	US-09-716-129-41
27	46.6	2.5	3116	4	US-09-311-021-187

28	46.4	2.5	258	4	US-09-621-976-15353	Sequence 15353, A
29	46.4	2.5	1172	1	US-07-945-288-9	Sequence 9, Appli
30	46.4	2.5	1172	1	US-08-462-831-9	Sequence 9, Appli
31	46.4	2.5	1172	1	US-08-461-809-9	Sequence 9, Appli
32	46.4	2.5	1172	1	US-08-461-441-9	Sequence 9, Appli
33	46.4	2.5	1172	5	PCT-US93-08518-9	Sequence 179, App
34	46.4	2.5	1509	3	US-09-149-476-179	Sequence 2, Appli
35	46.4	2.5	1738	2	US-08-379-482A-2	Sequence 14123, A
36	46.4	2.5	40323	4	US-09-949-016-14123	Sequence 14383, A
37	46.4	2.5	54950	4	US-09-949-016-14383	Sequence 11000, A
38	46.2	2.5	341	4	US-09-621-976-11000	Sequence 27, Appli
39	46.2	2.5	1872	3	US-09-291-922-27	Sequence 3, Appli
40	46	2.5	406	4	US-09-829-481-3	Sequence 11, Appli
41	46	2.5	1584	4	US-09-807-258-11	Sequence 5, Appli
42	46	2.5	1619	4	US-09-388-413B-5	Sequence 5, Appli
43	46	2.5	1619	4	US-10-233-745-5	Sequence 2, Appli
44	46	2.5	1653	3	US-09-345-469-2	Sequence 75, Appli
45	46	2.5	1825	3	US-09-461-697-75	

ALIGNMENTS

RESULT 1
US-09-471-276-571
; Sequence 571, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PATENT NO. 6822072
; FILE REFERENCE: GENSET 025CPI
; CURRENT APPLICATION NUMBER: US/09/471,276
; EARLIER FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 571
; LENGTH: 373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 276..371
; NAME/KEY: sig_peptide
; LOCATION: 276..335
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.09999990463257
; OTHER INFORMATION: seq LMCCSPSSRTSS/LS
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 251
; OTHER INFORMATION: n=a, g, c or t
; OTHER INFORMATION: Oligonucleotide
US-09-471-276-571

Query Match 7.4% Score 135.2; DB 4; Length 373;
Best Local Similarity 69.9%; Pred.No. 2.4e-26;
Matches 251; Conservative 5; Mismatches 10; Indels 93; Gaps 2;

Qy	1	CTGCAGCCAACCTTGTGGACATCTCGCAATGCTTGGAGCTCCTGCATAGAGAGCTTT	60
Db	4	CTGCAGCCAACCTTGTTCACCATCTCGCAATGCTTGGAGCTCCTGCATAGAG	57
Qy	61	TCCTTAGTGCCAGAGTCTGTGCACTCTGCGACTTCCTGAACCCCACTATCATGC	120

Db 58 -----AGTGCCACAGAGTCCTGGTAAACCTGTGGACTTCTGAAACCCCACTATSTG 111
 QY 121 GGCAGGTGTTCTTGGAAACCCAGACAAAGTGCCTCAGTCCAGAGCCAGCAGCAGCATG-- 178
 Db 112 GGCAGGTGTTCTTGGRRACCCAGACAAAGTGCCTCAGTCCAGAGCCAGCAGCAGTTTGTGTA 171
 QY 179 ----- 178
 Db 172 ACTGCGTTCTGACCTTGGCGGAGAACTCCAAAGAGTAGCCAGGCTGGRGGCTTCAGCC 231
 QY 179 -----CGGAGCTGTGGGGTTCAGCCGCTATGACACGAGGAGGA 219
 Db 232 GAGCTTACCGAGCAGCATNCGAGCTGTGGGTTCAGCCGCTATGACACGAGGAGGA 291
 QY 220 CTTCCTGTGTGTGTCAGAGCCCTTCTTCAGAAACATCCAGCTTCCCTGCTGGCGCTTG 278
 Db 292 CTTCCTGTGTGTGTCAGAGCCCTTCTTCAGAAACATCCAGCTTCCCTGCTGGCGGATG 350

RESULT 2
 US-09-270-767-12725
 ; Sequence 12725, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 12725
 ; LENGTH: 645
 ; TYPE: DNA
 ; ORGANISM: Drosophila melanogaster
 ; US-09-270-767-12725

Query Match 5.8%; Score 107.2; DB 4; Length 645;
 Best Local Similarity 56.2%; Pred. No. 1.2e-18;
 Matches 227; Conservative 0; Mismatches 168; Indels 9; Gaps 1;
 QY 464 CCAACTCTGTCCACAGCTCCGACAGCAGACATCAAGTGTGGCGCCCTGGGTGAC 523
 Db 112 CCACAGGTGTGATCGCTTGGACCCCGTACATCGATGTGATCGGAGCAATGGGTGAC 171
 QY 524 TCTCTGACTACAGCAGTGGAGCTCGACCAAACTCCAGTGACCTACCCACATCTGG 583
 Db 172 TCGCTGACCGCGGAACGGCATATTTGCGCAAACTTACTGTCATGTGACCGTGGAGAC 231
 QY 584 AGGGAGCTCTCTTGGAGCATTTGGAGGGATGGAACTTGGAGACTCACACACACTGGCC 643
 Db 232 AGGGGGTGTGTGGTCCATTTGGGGGCGAGTAGACTGAGGAGTACTTGAAGTGGCA 291
 QY 644 AACATCTGAAGAGTTCAACCTTACCTCTTGGCTTCTTA-----CGAGACC 694
 Db 292 AACATCTGAAGAGTTCAATCCCACTGTACCGCTATGCGATCAAGAGCGCATCTCG 351
 QY 695 TGGAGGGGACAGCAGACTAATGTGGCAGCGGAGGGCCAGAGCTAGGAGCATGGCA 754
 Db 352 ACGGACCGCTCTCGCGCTTGTGTCGCGAACTCGCGCCATGTCCAGGGATGCGG 411
 QY 755 GCCCAGCGCTGGGACCTGGTAGAGCGAATGAAACACAGCCCGACATCAACTGGAGAA 814
 Db 412 CACATGGCCAAGTCTCTGGTTCGCGCATGCAACGGGATCCGAGGGTGAACATGACCTCC 471
 QY 815 GACTGGAAGTGTGTCAGACTTCTTATTTGGGGTCAAGCACTTGTG 858
 Db 472 GACTGGAACTGGTCACTCTCTTCTTCAATGGCAACAGCACTTCTG 515

RESULT 3
 US-09-270-767-28539
 ; Sequence 28539, Application US/09270767

; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 28539
 ; LENGTH: 323
 ; TYPE: DNA
 ; ORGANISM: Drosophila melanogaster
 ; US-09-270-767-28539
 Query Match 3.4%; Score 62.2; DB 4; Length 323;
 Best Local Similarity 60.2%; Pred. No. 1.1e-06;
 Matches 103; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
 QY 688 CAGCAGCTGGGAGGACAGCAGGACTAAATGTGGCAGCGGAGGGCCAGAGCTAGGGA 747
 Db 23 CATCTGAGGACCGCTCTCGCGCTTCGATGTGCGCAACTGCGCGCCATGTCCAGGA 82
 QY 748 CATGCCAGCCAGGCTGGACCTGTAGAGCGCAATGAAACAGCCCGACATCAACT 807
 Db 83 TATGCCGACATGCGCAAGGTCTGTGTCGCGCATGCAACCGGATCCGAGGTGAACAT 142
 QY 808 GGAGAAAGACTGGAAGCTGTGTCACACTCTTTCATTTGGGTCAACGACTTGTG 858
 Db 143 GACCTCCGACTGGAAACTGTCTCACTCTTTCATTTGGCAACAGCACTTCTG 193

RESULT 4
 US-09-800-729-35
 ; Sequence 35, Application US/09800729
 ; Patent No. 6605592
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni et al.
 ; TITLE OF INVENTION: 32 Human secreted proteins
 ; FILE REFERENCE: P2044P1
 ; CURRENT APPLICATION NUMBER: US/09/800,729
 ; CURRENT FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: PCT/US00/26013
 ; PRIOR FILING DATE: 2000-09-22
 ; PRIOR APPLICATION NUMBER: 60/155,709
 ; PRIOR FILING DATE: 1999-09-24
 ; NUMBER OF SEQ ID NOS: 217
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 35
 ; LENGTH: 6065
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (6035)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: SITE
 ; LOCATION: (6037)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: SITE
 ; LOCATION: (6038)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; US-09-800-729-35

Query Match 2.7%; Score 49.6; DB 4; Length 6065;
 Best Local Similarity 80.6%; Pred. No. 0.014;
 Matches 58; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 QY 1764 GAATGGATACATTAAATAAGTCCAAAGCTATTTTAAAAAATAAAAAAAAAAAAAA 1823
 Db 5915 GAATGTATGTAGAAATAAAGTTGAAGATCTTTAAAAAATAAAAAAAAAAAAAA 5974
 QY 1824 AAAAAAAAAAAAAA 1835

Db 5975 AAAAAAAAAAAAAA 5986
|||||

RESULT 5

US-09-621-976-10543
; Sequence 10543, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 10543
; LENGTH: 193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 36..37
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-10543

Query Match 2.7%; Score 49.4; DB 4; Length 193;
Best Local Similarity 78.7%; Pred. No. 0.0023; Indels 0; Gaps 0;
Matches 59; Conservative 0; Mismatches 16;
Qy 1761 CTGGAATGGATACATTTAAATAAAGTCCAAAGCTATTATTAATAAAAAAAAAAAAAAAAAA 1820
Db 68 CTGGAATAAAGTCCAAAGCTATTATTAATAAAAAAAAAAAAAAAAAA 127
Qy 1821 AAAAAAAAAAAAAA 1835
Db 128 AAAAAAAAAAAAAA 142

RESULT 6

US-09-800-729-78
; Sequence 78, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-800-729-78

Query Match 2.6%; Score 48.2; DB 4; Length 1141;
Best Local Similarity 76.6%; Pred. No. 0.013; Indels 0; Gaps 0;
Matches 59; Conservative 0; Mismatches 18;
Qy 1759 TCCTGGAATGGATACATTTAAATAAAGTCCAAAGCTATTATTAATAAAAAAAAAAAAAAAAAA 1818
Db 1034 TCATGAATCAATACATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1093
Qy 1819 AAAAAAAAAAAAAA 1835
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Db 1094 AAAAAAAAAAAAAA 1110

RESULT 7

US-09-647-143-1
; Sequence 1, Application US/09647143
; Patent No. 6680196
; GENERAL INFORMATION:
; APPLICANT: Batra, Surinder K.
; APPLICANT: Hollingsworth, Michael A.
; APPLICANT: University of Nebraska Board of Regents
; TITLE OF INVENTION: No. 6680196el Gene That is Amplified and
; FILE REFERENCE: Overexpressed in Cancer and Methods of Use Thereof
; CURRENT APPLICATION NUMBER: US/09/647,143
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US99/06633
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,649
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1937
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-647-143-1

Query Match 2.6%; Score 48.2; DB 4; Length 1937;
Best Local Similarity 86.9%; Pred. No. 0.018; Indels 0; Gaps 0;
Matches 53; Conservative 0; Mismatches 8;
Qy 1775 TTTAAATAAAGTCCAAAGCTATTATTAATAAAAAAAAAAAAAAAAAA 1834
Db 1867 TGTATATAAGTCACTTCTTTATAAAAAAAAAAAAAAAAAA 1926
Qy 1835 A 1835
Db 1927 A 1927

RESULT 8

US-09-800-729-11
; Sequence 11, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 2329
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-800-729-11

Query Match 2.6%; Score 48.2; DB 4; Length 2329;
Best Local Similarity 76.6%; Pred. No. 0.02; Indels 0; Gaps 0;
Matches 59; Conservative 0; Mismatches 18;
Qy 1759 TCCTGGAATGGATACATTTAAATAAAGTCCAAAGCTATTATTAATAAAAAAAAAAAAAAAAAA 1818
Db 2222 TCCTGGAATAGTTTTTCTAAATGGAATAAAGTCTTTTATAAAAAAAAAAAAAAAAAA 2281
Qy 1819 AAAAAAAAAAAAAA 1835
|||||

us-09-778-961-1.rni

Mon Mar 28 09:43:24 2005

QY 1774 ATTTAAATAAGTCCAAAGCTATTTTAAAAA 1833
 Db 1900 ATTGAATAAAAAATTTTAAAAA 1959
 QY 1834 AA 1835
 Db 1960 AA 1961

Db 2282 AAAAAAAAAAAAAA 2298

RESULT 9
 US-09-800-729-27
 ; Sequence 27, Application US/09800729
 ; Patent No. 6605592
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni et al.
 ; TITLE OF INVENTION: 32 Human secreted proteins
 ; FILE REFERENCE: P2044PI
 ; CURRENT APPLICATION NUMBER: US/09/800,729
 ; CURRENT FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: PCT/US00/26013
 ; PRIOR FILING DATE: 2000-09-22
 ; PRIOR APPLICATION NUMBER: 60/155,709
 ; PRIOR FILING DATE: 1999-09-24
 ; NUMBER OF SEQ ID NOS: 217
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 27
 ; LENGTH: 2355
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (15)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: SITE
 ; LOCATION: (22)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: SITE
 ; LOCATION: (28)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; US-09-800-729-27

Query Match 2.6%; Score 48.2; DB 4; Length 2355;
 Best Local Similarity 76.6%; Pred. No. 0.02;
 Matches 59; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
 QY 1759 TCTGGAATGGATACATTTAAATAAGTCCAAAGCTATTTTAAAAA 1818
 Db 2258 TCTGGAATGGATTTTCTTAAATGTAATAAAGTCTTTTATATAA 2317

QY 1819 AAAAAAAAAAAAAA 1835
 Db 2318 AAAAAAAAAAAAAA 2334

RESULT 10
 US-09-920-759-10
 ; Sequence 10, Application US/09920759
 ; Patent No. 6537811
 ; GENERAL INFORMATION:
 ; APPLICANT: Brenda F. Baker
 ; APPLICANT: Susan M. Freier
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF SAP-1 EXPRESSION
 ; FILE REFERENCE: RTS-0267
 ; CURRENT APPLICATION NUMBER: US/09/920,759
 ; CURRENT FILING DATE: 2001-08-01
 ; NUMBER OF SEQ ID NOS: 91
 ; SEQ ID NO 10
 ; LENGTH: 1976
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (150)...(1367)
 ; US-09-920-759-10

Query Match 2.6%; Score 47.6; DB 4; Length 1976;
 Best Local Similarity 85.5%; Pred. No. 0.026;
 Matches 53; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

RESULT 11
 US-09-370-473-5
 ; Sequence 5, Application US/09370473
 ; Patent No. 6271031
 ; GENERAL INFORMATION:
 ; APPLICANT: Falco, S. Carl
 ; APPLICANT: Famodu, Layo O.
 ; APPLICANT: Rafalski, J. Antoni
 ; TITLE OF INVENTION: Quinolinate Metabolism Enzymes
 ; FILE REFERENCE: BB-1209
 ; CURRENT APPLICATION NUMBER: US/09/370,473
 ; CURRENT FILING DATE: 1999-08-09
 ; EARLIER APPLICATION NUMBER: 60/096,240
 ; EARLIER FILING DATE: August 12, 1998
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 5
 ; LENGTH: 2065
 ; TYPE: DNA
 ; ORGANISM: Triticum aestivum
 ; US-09-370-473-5

Query Match 2.6%; Score 47.2; DB 3; Length 2065;
 Best Local Similarity 72.6%; Pred. No. 0.034;
 Matches 61; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 QY 1752 CCTATGCTCCTGGAATGGATACATTTTAAATAAGTCCAAAGCTATTTTAAAAA 1811
 Db 1790 CCTATGCTCATTTTAAAAA 1849
 QY 1812 AAAAAAAAAAAAAA 1835
 Db 1850 AAAAAAAAAAAAAA 1873

RESULT 12
 US-09-620-312D-861
 ; Sequence 861, Application US/09620312D
 ; Patent No. 6569662
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Xue, Aidong J.
 ; APPLICANT: Yang, Yonghong
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Ma, Yunqing
 ; APPLICANT: Wang, Dunrui
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: John Tillinghaast
 ; APPLICANT: Drmanac, Radoje T.
 ; TITLE OF INVENTION: Polypeptides
 ; FILE REFERENCE: 784CIP2B
 ; CURRENT APPLICATION NUMBER: US/09/620,312D
 ; CURRENT FILING DATE: 2000-07-19
 ; PRIOR APPLICATION NUMBER: 09/552,317
 ; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 861
; LENGTH: 4494
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (207)..(3002)
US-09-620-312D-861

Query Match 2.6%; Score 47.2; DB 4; Length 4494;
Best Local Similarity 86.7%; Pred. No. 0.053;
Matches 52; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 1776 TTAATAAGTCCAAAGCTATTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1835
Db 4421 TTTAATAAGTCTATGTGATTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4480

RESULT 13
US-09-621-976-12892
; Sequence 12892, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.Pm
; SEQ ID NO 12892
; LENGTH: 130
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-12892

Query Match 2.6%; Score 47; DB 4; Length 130;
Best Local Similarity 78.9%; Pred. No. 0.0082;
Matches 56; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Qy 1765 AATCGATACATTTAAATAAGTCCAAAGCTATTTTAAAAAAAAAAAAAAAAAAAA 1824
Db 13 AAAGGAGACATGTATAA 72
Qy 1825 AAAAAAAAAA 1835
Db 73 AAAAAAAAAA 83

RESULT 14
US-09-949-016-161396/c
; Sequence 161396, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 161396
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-161396

Query Match 2.6%; Score 47; DB 4; Length 601;
Best Local Similarity 71.3%; Pred. No. 0.019;
Matches 62; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
Qy 1748 CAGCCTATGCTCTCGAATGGATACATTTAAATAAGTCCAAAGCTATTTTAAAA 1807
Db 205 CAGGAGTTTGAGACTGGCTGGCCACATGCGCAAAACCCCATCTACTAAAAAAA 146
Qy 1808 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1834
Db 145 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 119

RESULT 15
5498694-3
; Patent No. 5498694
; APPLICANT: ROUSLAHTI, ERKKI I.
; TITLE OF INVENTION: PEPTIDES OF THE CYTOPLASMIC DOMAIN OF
; INTEGRIN
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,967
; FILING DATE: 10-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 973,547
; FILING DATE: 09-NOV-1992
; APPLICATION NUMBER: 357,824
; FILING DATE: 25-MAY-1989
; SEQ ID NO:3
; LENGTH: 688
5498694-3

Query Match 2.6%; Score 47; DB 6; Length 688;
Best Local Similarity 78.9%; Pred. No. 0.021;
Matches 56; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Qy 1765 AATCGATACATTTAAATAAGTCCAAAGCTATTTTAAAAAAAAAAAAAAAAAAAA 1824
Db 587 AATAATAATAATAATAATAATAATAATAATAAGTTACTTCCAAAAAAAAAAAA 646
Qy 1825 AAAAAAAAAA 1835
Db 647 AAAAAAAAAA 657

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22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

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SUMMARIES

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3	1421	77.4	4425	17	US-10-092-900A-85
4	1362	74.2	4377	13	US-10-054-691-1
5	1231.8	67.1	4268	17	US-10-092-900A-81
6	667.4	36.4	802	17	US-10-276-774-73
7	667.4	36.4	802	17	US-10-296-115-600
8	575	31.3	861	17	US-10-264-237-323
9	396.2	21.6	572	10	US-09-764-891-1391
10	210.6	11.5	1624	17	US-10-092-900A-83
11	186.8	10.2	2477	17	US-10-094-749-390
					Sequence 19, Appl
					Sequence 11, Appl
					Sequence 85, Appl
					Sequence 1, Appl
					Sequence 81, Appl
					Sequence 73, Appl
					Sequence 600, Appl
					Sequence 323, Appl
					Sequence 1391, Appl
					Sequence 83, Appl
					Sequence 390, Appl

ALIGNMENTS

RESULT 1

US-10-478-245-19

; Sequence 19, Application US/10478245

; Publication No. US20040171009A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;

; APPLICANT: YUE, Henry; AZIMZAI, Yalda;

; APPLICANT: BAUGHN, Mariah R.; BURFORD, Neil;

; APPLICANT: REDDY, Roopa; CHAWLA, Narinder K.;

; APPLICANT: DAS, Debopriya; NGUYEN, Dannel B.;

; APPLICANT: YAO, Monique G.; ARVIZU, Chandra S.;

; APPLICANT: LU, Yan; GANDHI, Ameena R.;

; APPLICANT: GRIFFIN, Jennifer A.; ELLIOTT, Vicki S.;

; APPLICANT: RAMKUMAR, Jayalaxmi; LAL, Preeti G.;

; APPLICANT: LU, Dyrung Aina M.; LEE, Ernestine A.;

; APPLICANT: LEE, Soo Y.; YUE, Huibin;

; APPLICANT: YANG, Junming; TRIBOULEY, Catherine M.;

; APPLICANT: KABLE, Amy B.; SWARNAKAR, Anita;

; TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES

; FILE REFERENCE: PI-0427 USN

; CURRENT APPLICATION NUMBER: US/10/478,245

; CURRENT FILING DATE: 2003-11-18

; PRIOR APPLICATION NUMBER: PCT/US02/15688

; PRIOR FILING DATE: 2002-05-17

; PRIOR APPLICATION NUMBER: US 60/292,242

; PRIOR FILING DATE: 2001-05-18

; PRIOR APPLICATION NUMBER: US 60/293,726

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/295,346

; PRIOR FILING DATE: 2001-06-01

; PRIOR APPLICATION NUMBER: US 60/303,404

; PRIOR FILING DATE: 2001-07-06

; PRIOR APPLICATION NUMBER: US 60/314,754

; PRIOR FILING DATE: 2001-08-24

Sequence 257, App

Sequence 52985, A

Sequence 126452,

Sequence 3816, Ap

Sequence 7744, App

Sequence 526, App

Sequence 49109, A

Sequence 68350, A

Sequence 32674, A

Sequence 9532, Ap

Sequence 8191, Ap

Sequence 10381, A

Sequence 115890,

Sequence 1677, Ap

Sequence 8193, Ap

Sequence 16188, A

Sequence 16650, A

Sequence 66929, A

Sequence 78265, A

Sequence 56643, A

Sequence 303, App

Sequence 4408, Ap

Sequence 139428,

Sequence 71, Appl

Sequence 483, App

Sequence 71, Appl

Sequence 71, Appl

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Sequence 483, App

Sequence 483, App

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; PRIOR APPLICATION NUMBER: US 60/351,262
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/368,799
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 4424
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7504684CB1
; US-10-478-245-19

Query Match      89.9%; Score 1649.2; DB 18; Length 4424;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 1731; Conservative 0; Mismatches 68; Indels 21; Gaps 2;

Qy 1 CTGAGCCAACTTTGTTGACCATCTCCGCAATGCTTGGACGTCCTGGCATAGAGAGCTTT 60
Db 2626 CTGAGCCAACTTTGTTGACCATCTCCGCAATGCTTGGACGTCCTGGCATAGAGAG 60

Qy 61 TCCCTTAGGTGCCAGAGTCTCGTCAACCTCGTGAACCTTCTGAACCCCACTATCATGC 120
Db 2680 -----AGGTGCCAGAGTCTCGTCAACCTCGTGAACCTTCTGAACCCCACTATCATGC 120

Qy 121 GGCAGGTGTTCTGGGAACCCAGACAGTGGCCAGTGCAGGAGGCGCAGAGCATGGC 180
Db 2734 GGCAGGTGTTCTGGGAACCCAGACAGTGGCCAGTGCAGGAGGCGCAGAGCATGGC 180

Qy 181 CGAGCTGTTGGGTGAGGCGCTATGACACGACGAGGAGTCTCTGTGTGTGTGTGAGCC 240
Db 2785 TGGGCTCCCATAGTCTCTTTTGGCCAGAGTGCATCCACCAATCAGAAATTCGA 2844

Qy 241 CTCTTTCAGAAATCAGAGTCCCTCTGCTGGGCTTGAACCACTTGGAGCAAAACAGA 300
Db 2845 CTCCAGCTGGCCAGAGGCTTGGACCAATATGCTTGAACCACTTGGAGCAAAACAGA 3004

Qy 301 GACCTGGACCTGAGCAGAGATGCCCATCACTGTGCCCTCCCACTCAGAAATGAGCCCTTCT 360
Db 2905 GACCTGGACCTGAGCAGAGATGCCCATCACTGTGCCCTCCCACTCAGAAATGAGCCCTTCT 3604

Qy 361 GAGAACCCCTCGGAATAGTAATACTACAGTACCCATCAAGCAGGCAATGAGACTGGG 420
Db 2965 GAGAACCCCTCGGAATAGTAATACTACAGTACCCATCAAGCAGGCAATGAGAACTGGG 3024

Qy 421 CAGTGACTTCTGTGTACAGAGTGAAGCTTCCCAATAGTGTTCACACTCTGTCCACCA 480
Db 3025 CAGTGACTTCTGTGTACAGAGTGAAGCTTCCCAATAGTGTTCACACTCTGTCCACCA 3084

Qy 481 GCTCCGACAGCAGACATCAAAAGTGTGGCGCCCTGGGTGACTCTCTGACTACAGCAGT 540
Db 3085 GCTCCGACAGCAGACATCAAAAGTGTGGCGCCCTGGGTGACTCTCTGACTACAGCAGT 3144

Qy 541 GGGAGCTGNCAGAACTCCAGTGACCTACCACTCTTGGAGGGGACTCTCTTGGAG 600
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Qy 601 CATTTGAGGGGATGGGAATTGGAGACTCACAACCACTGCCCCAATCTTGAAGAAGTT 660
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Qy 721 GGCAGCGGAGGGGCCAGAGCTAGGACATGCGAGCCCGAGGCTGGGACTGGTAGCG 780
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Qy 781 AATCAAAAAACAGCCCGACATCAACCTGGAGAAAGCTGGAAGCTGGTCACTTTCAT 840

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3385 AATGAAAAACAGCCCGACATCACTGGAGAAAGACTGGAAGCTGGTCACTCTTCAT 3444
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3445 TGGGGTCAACGACTTTGTGTATTACTGTGAGAAATCCGAGGCCCACTTTGGCCACGGAATA 3504
901 TGTTCAGCAGATCCCAAGCCCTGGACATCTCTCTGAGGAGCTCCCAAGGGCTTTGCT 960
3505 TGTTCAGCAGATCCCAAGCCCTGGACATCTCTCTGAGGAGCTCCCAAGGGCTTTGCT 3564
961 CAACGTGTGGAGTCAATGGAGCTGGCTAGCTGTATACAGGCGCAAGGGCGGAATGTGC 1020
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1021 CATGTGGAGCTCAGAACTGCACTGCTGCTGACACTCGACACTCGCAAGCTCCCTGGAGAA 1080
3625 CATGTGGAGCTCAGAACTGCACTGCTGCTGACACTCGACACTCGCAAGCTCCCTGGAGAA 3684
1081 GCAGAACTCAAGAAAGTGAACCTGGAACCTTCCAGCATGGCATCTCCAGTTTCTCTACTG 1140
3685 GCAGAACTCAAGAAAGTGAACCTGGAACCTTCCAGCATGGCATCTCCAGTTTCTCTACTG 3744
1141 GCACCAATACACAGCGTGAAGACTTTGGGTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1200
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1201 ACTCACTTCTCAGACCGCGGCAATGCGGATGGCCATCGCACTCTGGAACCAACATGCTGGA 1260
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1261 TCACCTTCTCAGACCGCGGCAATGCGGATGGCCATCGCACTCTGGAACCAACATGCTGGA 1320
3865 TCACCTTCTCAGACCGCGGCAATGCGGATGGCCATCGCACTCTGGAACCAACATGCTGGA 3924
1321 ACCAGTGGGCGGCAAGTACTCTCAACCACTTCAACCAAGCGGAGCCCAAACTCAAGT 1380
3925 ACCAGTGGGCGGCAAGTACTCTCAACCACTTCAACCAAGCGGAGCCCAAACTCAAGT 3984
1381 CCCCTCTCTGAGAGCCCTTACCTCTACACCTCGGAAACAGCCGANTGCTCCAGACCA 1440
3985 CCCCTCTCTGAGAGCCCTTACCTCTACACCTCGGAAACAGCCGANTGCTCCAGACCA 4044
1441 GGCTGAAGAGCCCGGAGGTGCTCTACTGGGCTGTCCAGTGGCAGCGGAGTGGGCT 1500
4045 GGCTGAAGAGCCCGGAGGTGCTCTACTGGGCTGTCCAGTGGCAGCGGAGTGGGCT 4104
1501 TGTGTGGGATCATCGGAGCAGTGTCTGAGGTGCAAGGAGAGGTGGCCGAGGAGAGA 1560
4105 TGTGTGGGATCATCGGAGCAGTGTCTGAGGTGCAAGGAGAGGTGGCCGAGGAGAGA 4164
1561 TCCTCAATGAGCTGCGGACTGTGGCCCTCTAGGCCCGGGGTGGGTCTTCACTCACTAAA 1620
4165 TCCTCAATGAGCTGCGGACTGTGGCCCTCTAGGCCCGGGGTGGGTCTTCACTCACTAAA 4224
1621 CTCCTTATAGCCACTCTCTTCACTGGCTCTGCCCCCAGCCACTCCCGGCGCAGGAGAT 1680
4225 CTCCTTATAGCCACTCTCTTCACTGGCTCTGCCCCCAGCCACTCCCGGCGCAGGAGAT 4284
1681 GCTTCAATGCTGTGGTGGCAGAGCCCGAGGAGCAGTCAAACTTCTTGGGGCTGGG 1740
4285 GCTTCAATGCTGTGGTGGCAGAGCCCGAGGAGCAGTCAAACTTCTTGGGGCTGGG 4344
1741 CTTTCTTCCAGGCTATGCTCTTGGAAATGATATTAATTAATTAATTAATTAATTAATTAAT 1800
4345 CTTTCTTCCAGGCTATGCTCTTGGAAATGATATTAATTAATTAATTAATTAATTAATTAAT 4404
1801 AAAAAAATAAAAAAAAAA 1820
4405 AAAAAAATAAAAAAAAAA 4424

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; Sequence 11, Application US/10478245
; Publication No. US20040171009A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;
; APPLICANT: YUE, Henry; AZIMZAI, Yalda;
; APPLICANT: BAUGHN, Mariah R.; BURFORD, Neil;
; APPLICANT: REDDY, Roopa; CHAWLA, Narinder K.;
; APPLICANT: DAS, Debopriya; NGUYEN, Darniel B.;
; APPLICANT: YAO, Monique G.; ARVIZU, Chandra S.;
; APPLICANT: LU, Yan; GANDHI, Ameena R.;
; APPLICANT: GRIFFIN, Jennifer A.; ELLIOTT, Vicki S.;
; APPLICANT: RAMKUMAR, Jayalaxmi; LAL, Preeti G.;
; APPLICANT: LU, Dyung Aina M.; LEE, Ernestine A.;
; APPLICANT: LEE, Soo Y.; YUE, Huibin;
; APPLICANT: YANG, Junning; TRIBOULEY, Catherine M.;
; APPLICANT: KABLE, Amy E.; SWARNAKAR, Anita
; TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES
; FILE REFERENCE: PI-0427 USN
; CURRENT APPLICATION NUMBER: US/10/478,245
; PENDING FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/15688
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/292,242
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/293,726
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/295,346
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/303,404
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 60/314,754
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/351,262
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/368,799
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 4607
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 2440624CB1
US-10-478-245-11

Query Match 84.8%; Score 1555.2; DB 18; Length 4607;
Best Local Similarity 90.2%; Pred. No. 0;
Matches 1799; Conservative 0; Mismatches 3; Indels 192; Gaps 5;

Qy 1 CTGCAGCCCACTTTGTTGACCATCTCCGCAATGCTTGGAGCTCTGCATAGAGACTTT 60
Db 2626 CTGCAGCCCACTTTGTTGACCATCTCCGCAATGCTTGGAGCTCTGCATAGAG----- 2679

Qy 61 TCCCTTAGTGCCCGCAGAGTCTCGTGTCACTCTGAGCTTCTGAACCCCACTATCATGC 120
Db 2680 -----AGGTGCCCGAGAGTCTCGTGTCACTCTCGTGTGACTTCTTGAACCCCACTATCATGC 2733

Qy 121 GGCAGGTGTTCTTGGGAAACCCAGACAAAGTCCCGCAGTGCAGCAGGCCA----- 168
Db 2734 GGCAGGTGTTCTTGGGAAACCCAGACAAAGTCCCGCAGTGCAGCAGGCCAGCGTTTGTGTA 2793

Qy 169 ----- 168
Db 2794 ACTGGTTCTGACCCCTGGGGGAGAACTCCCAAGAGCTAGCCAGGCTGGAGGCCCTTCAGCC 2853

Qy 169 -----GAGCAGCATGCGCAGCTGTGGGGTTCAGGCCGCTATGACACGCGAGG 218
Db 2854 GAGCCTACCGGAGCAGCATGCGCAGCTGTGGGGTTCAGGCCGCTATGACACGCGAGG 2913

Qy 219 ACTTCTGTGGTGTGAGCCCTTTCTTCCAGAAATCCAGCTCCCTGCTCTGCTGCTGCT 273
Db 4053 TCACCCCACTGAAACGAGAGAGGGGACACTGACCTCACCTTCTTCTCCGAGACTGTTTTC
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Db	4013	AACAGTGGGGCCGCAAGACTACTCTCCAAACATTTACCCACAGCCGAGCCAAACTCAAGT	4073
Qy	1380	GCCCTCTCTCTGAGAGCCCTTACCTCTACACCCCTGCGGAAACAGCCGATTCCTCCAGACC	1439
Db	4073	GCCCTCTCTCTGAGAGCCCTTACCTCTACACCCCTGCGGAAACAGCCGATTCCTCCAGACC	4132
Qy	1440	AGGCTGAAGAAGCCGCCAGAGTGTCTACCTGGGGTGTCCAGTGGGACAGCGGAGTGGGCC	1499
Db	4133	AGGCTGAAGAAGCCGCCAGAGTGTCTACCTGGGGTGTCCAGTGGGACAGCGGAGTGGGCC	4192
Qy	1500	TTGTGGTGGGCATCATCGGACACAGTGGTCTGGAGGTGCAGAGAGGTGGCCGAGGGAAG	1559
Db	4193	TTGTGGTGGGCATCATCGGACACAGTGGTCTGGAGGTGCAGAGAGGTGGCCGAGGGAAG	4252
Qy	1560	ATCTCCAAATGAGCTGCGCACTGTGGCCCTCTAGGCCCGGGGGTGGTCTCTCACCCCTAA	1619
Db	4253	ATCTCCAAATGAGCTGCGCACTGTGGCCCTCTAGGCCCGGGGGTGGTCTCTCACCCCTAA	4312
Qy	1620	ACTCCCTATAGGCACCTCTCTTCACGGCCCTCTGCCCGAGCCACTCCCGGCCACAGGACA	1679
Db	4313	ACTCCCTATAGGCACCTCTCTTCACGGCCCTCTGCCCGAGCCACTCCCGGCCACAGGACA	4372
Qy	1680	TGCTTCAATGCCGTGGTGCATAGAGGCCAGGGGACAGTCAACTCTCTGG	1732
Db	4373	TGCTTCAATGCCGTGGTGCATAGAGGCCAGGGGACAGTCAACTCTCTGG	4425

RESULT 4

US-10-054-691-1

; Sequence 1, Application US/10054691

; Publication No. US20020115846A1

; GENERAL INFORMATION:

; APPLICANT: Yu, Xuanchuan

; APPLICANT: Miranda, Maricar

; APPLICANT: Turner, C. Alexander Jr.

; TITLE OF INVENTION: No. US20020115846A1 Human Lipase and Polynucleotides

; FILE OF INVENTION: No. US20020115846A1

; CURRENT APPLICATION NUMBER: US/10/054,691

; CURRENT FILING DATE: 2001-01-22

; PRIOR APPLICATION NUMBER: US 60/264,049

; PRIOR FILING DATE: 2001-01-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 4377

; TYPE: DNA

; ORGANISM: homo sapiens

US-10-054-691-1

Query Match	74.2%	Score 1362;	DB 13;	Length 4377;
Best Local Similarity	89.3%	Pred. No. 0;		
Matches 1582;	Conservative 0;	Mismatches 0;	Indels 190;	Gaps 3;
Qy	1	CTGCAGCCAACTTTGTTGACCAATCTCGGAAATGCTTGGACGTCTCGCAATAGCCTTGGACGTCTGCAATAGAGACTTT	60	
Db	2618	CTGCAGCCAACTTTGTTGACCAATCTCGGAAATGCTTGGACGTCTCGCAATAGCCTTGGACGTCTGCAATAGAGACTTT	2671	
Qy	61	TCCTTAGGTGGCCAGAGTCTGGTCAAACCTGCTGACATCTCTGAAACCCCACTATCATGC	120	
Db	2672	-----AGGTGGCCAGAGTCTGGTCAAACCTGCTGACATCTCTGAAACCCCACTATCATGC	2725	
Qy	121	GGCAGGTGTTCTTGGGAAACCCAGACAAGTGCCAGTGCCAGCAGGCA	168	
Db	2726	GGCAGGTGTTCTTGGGAAACCCAGACAAGTGCCAGTGCCAGCAGGCA	2785	
Qy	169	-----	168	
Db	2786	ACTGCGTTCTGACCTGCGGAGAACTCCCAAGAGCTAGCAGGCTGGAGGCTTCAGCC	2845	
Qy	169	-----GACAGCATGCGGAGCTGGTGGGTCAGGCCCGCTATGACACGAGGAGG	218	
Db	2846	GAGCCTACCGGAGCAGCATGCGGAGCTGGTGGGTCAGGCCCGCTATGACACGAGGAGG	2905	

QY	219	ACTTCTCTGTGTGCTGCAGCCCTTCTTCCAGAACATCCAGCTCCCTGTCTCTGGC-----	273
DB	2906	ACTTCTCTGTGTGCTGCAGCCCTTCTTCCAGAACATCCAGCTCCCTGTCTCTGGCGGATG	2965
QY	274	-----	273
DB	2966	GGCTCCAGATACGTCTCTTTTGCCCCAGACTGCATCCACCCAAATTCAGAAATTCCTACT	3025
QY	274	-----GCTTGAACCACTTTGGAAGCAAAACAGAGA	302
DB	3026	CCAGCTGGCCAGAGCCCTTTGGACCAATATGCTTGAACCACTTGGAAAGCAAAACAGAGA	3085
QY	303	CCCTGGACCTGAGAGAGAGATGCCCATCACTGTCCCACTCAGAAATGAGCCCTTCTCTCA	362
DB	3086	CCCTGGACCTGAGAGAGAGATGCCCATCACTGTCCCACTCAGAAATGAGCCCTTCTCTCA	3145
QY	363	GNACCCCTGGAAATGTAATACAGTATACCCCATCAAGCCAGACCATTTGAGAACTGGGGCA	422
DB	3146	GAACCCCTCGGAATAGTAATACAGTATACCCCATCAAGCCAGACCATTTGAGAACTGGGGCA	3205
QY	423	GTGACTCTCTGTGTACAGAGTGAAGGCTTCCAAATAGTGTCCAACTCTGTCCACCAGC	482
DB	3206	GTGACTCTCTGTGTACAGAGTGAAGGCTTCCAAATAGTGTTCCAAACCTCTGTCCACCAGC	3265
QY	483	TCCGACACAGACATCAAAAGTGGTGGCCGCCCTGGGTGACTCTCTGACTACAGCAGTGG	542
DB	3266	TCCGACACAGACATCAAAAGTGGTGGCCGCCCTGGGTGACTCTCTGACTACAGCAGTGG	3325
QY	543	GAGCTCGAACCAACAACTCCAGTGACTACCCACATCTTGGAGGGGACTCTCTTTGGAGCA	602
DB	3326	GAGCTCGAACCAACAACTCCAGTGACTACCCACATCTTGGAGGGGACTCTCTTTGGAGCA	3385
QY	603	TTGGAGGGGATGGGAACTTGGAGACTCACACCACTGCCCCAACATCTGAGAAAGTTCA	662
DB	3386	TTGGAGGGGATGGGAACTTGGAGACTCACACCACTGCCCCAACATCTGAGAAAGTTCA	3445
QY	663	ACCTTTACTCTCTTGGCTTCTTACCAGACCTGGGAGGGGACAGCAGACTTAATATGTG	722
DB	3446	ACCTTTACTCTCTTGGCTTCTTACCAGACCTGGGAGGGGACAGCAGACTTAATATGTG	3505
QY	723	CAGCGGAAAGGGCCAGAGCTAGGACATGCCAGCCAGGCTGGGACCTGGTAGAGCGAA	782
DB	3506	CAGCGGAAAGGGCCAGAGCTAGGACATGCCAGCCAGGCTGGGACCTGGTAGAGCGAA	3565
QY	783	TGAAAAACAGCCCCGACATCAACTGGAGAAAGACTGGAAGCTGTGTACACTTCTCATTTG	842
DB	3566	TGAAAAACAGCCCCGACATCAACTGGAGAAAGACTGGAAGCTGTGTACACTTCTCATTTG	3625
QY	843	GGGTCAACGACTTGTGTCAATTACTGTGAGAAATCCGAGGCCCACTTGGGCCACGGAAATG	902
DB	3626	GGGTCAACGACTTGTGTCAATTACTGTGAGAAATCCGAGGCCCACTTGGGCCACGGAAATG	3685
QY	903	TTCAGCACATCCAAAGGCCCTGGACATCTCTCTGAGGAGCTCCCAAGGGCTTTCGTCA	962
DB	3686	TTCAGCACATCCAAAGGCCCTGGACATCTCTCTGAGGAGCTCCCAAGGGCTTTCGTCA	3745
QY	963	ACGTGTGGAGGTCTATGGAGCTGGCTAGCTGTATACAGGGGCCAAGGCGGGAATGTGCCA	1022
DB	3746	ACGTGTGGAGGTCTATGGAGCTGGCTAGCTGTATACAGGGGCCAAGGCGGGAATGTGCCA	3805
QY	1023	TGCTGGCAGCTCAGAACACTGCATTTGCTCTCAGACACTCCGAAAGCTCCCTCGGAAAGC	1082
DB	3806	TGCTGGCAGCTCAGAACACTGCATTTGCTCTCAGACACTCCGAAAGCTCCCTCGGAAAGC	3865
QY	1083	AAGAACTGAAAGAAAGTGAATCGSAACTCCAGCATGGCATCTCCAGTTTCTCTCTACTGGC	1142
DB	3866	AAGAACTGAAAGAAAGTGAATCGSAACTCCAGCATGGCATCTCCAGTTTCTCTCTACTGGC	3925
QY	1143	ACCAATACACACAGCGTGAAGCTTTGCGGTTGTGGTGAGCTCTTCTTCCAAACACAC	1202
DB	3926	ACCAATACACACAGCGTGAAGCTTTGCGGTTGTGGTGAGCTCTTCTTCCAAACACAC	3985
QY	1203	TCAGCCCACTGAACGAGAGAGGGGACACTGACCTCACTTCTTCTCGAGGACTGTTTC	1262

Db	3986	TACCCCACTGAACGAGAGGGGACACTGACCTCACCTTCTTCCGAGGACTGTTTC	4045
QY	1263	ACTTCTCAGACCGCGGCATGCCAGATGGCCATCGCACTCTGGAAACAACATGCTGGAAC	1322
Db	4046	ACTTCTCAGACCGCGGCATGCCAGATGGCCATCGCACTCTGGAAACAACATGCTGGAAC	4105
QY	1323	CAGTGGGCGCGCAAGACTACTCTCCAAACAATTCAACACAGCGAGCCAACTCAAGTGCC	1382
Db	4106	CAGTGGGCGCGCAAGACTACTCTCCAAACAATTCAACACAGCGAGCCAACTCAAGTGCC	4165
QY	1383	CCTCTCTGAGAGCCCTTACCTTACACCTCGGAAACAGCCGATTCCTCCAGACCAGG	1442
Db	4166	CCTCTCTGAGAGCCCTTACCTTACACCTCGGAAACAGCCGATTCCTCCAGACCAGG	4225
QY	1443	CTGAAGAAGCCCGCAGGTGCTCTACTTGGGCTGTCCAGTGGCAGCGGAGTGGGCTTG	1502
Db	4226	CTGAAGAAGCCCGCAGGTGCTCTACTTGGGCTGTCCAGTGGCAGCGGAGTGGGCTTG	4285
QY	1503	TGTTGGGCATCATCGGACAGTGGTCTGAGAGTGCAGGAGAGTGGCCGAGGGAAGATC	1562
Db	4286	TGTTGGGCATCATCGGACAGTGGTCTGAGAGTGCAGGAGAGTGGCCGAGGGAAGATC	4345
QY	1563	CTCCAATGAGCTGCGCACTGTGGCCCTCTAG	1594
Db	4346	CTCCAATGAGCTGCGCACTGTGGCCCTCTAG	4377

RESULT 5

US-10-092-900A-81

Sequence 81, Application US/10092900A

Publication No. US20040043382A1

GENERAL INFORMATION:

APPLICANT: Padigar, Muralidhara

APPLICANT: Spytek, Kimberly A.

APPLICANT: Shenoy, Suresh G.

APPLICANT: Taupier Jr., Raymond J.

APPLICANT: Pena, Carol E.A.

APPLICANT: Li, Li

APPLICANT: Zerhusen, Bryan D.

APPLICANT: Gusev, Vladimir Y.

APPLICANT: Ji, Weizhen

APPLICANT: Gorman, Linda

APPLICANT: Miller, Charles E.

APPLICANT: Kekuda, Ramesh

APPLICANT: Patturajan, Meera

APPLICANT: Gangolli, Esha A.

APPLICANT: Vernet, Corine A.M.

APPLICANT: Guo, Xiaojia Sasha

APPLICANT: Tchernev, Velizar T.

APPLICANT: Fernandes, Elma R.

APPLICANT: Casman, Stacie J.

APPLICANT: Malvankar, Uriel M.

APPLICANT: Gerlach, Valerie

APPLICANT: Liu, Yi

APPLICANT: Anderson, David W.

APPLICANT: Spaderna, Steven K.

APPLICANT: Catterton, Elina

APPLICANT: Leite, Mario W.

APPLICANT: Zhong, Haihong

APPLICANT: Alsbrook, John P.

APPLICANT: Lepley, Denise M.

APPLICANT: Rieger, Daniel K.

APPLICANT: Burgess, Catherine E.

FILE OF INVENTION: No. US20040043382A1

TITLE REFERENCE: 21402-290C

CURRENT APPLICATION NUMBER: US/10/092,900A

PRIOR FILING DATE: 2002-03-07

PRIOR APPLICATION NUMBER: USN 60/274,322

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: USN 60/283,675

PRIOR FILING DATE: 2001-04-13

PRIOR APPLICATION NUMBER: USN 60/338,092

RESULT 5

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US-10-092-900A-81
; Sequence 81: Application US/10092900A
; Publication No. US20040043382A1
;
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esna A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haibong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Riedger, Daniel K.
; APPLICANT: Burgess, Catherine E.
;
; TITLE OF INVENTION: No. US2004004338
; FILE REFERENCE: 21402-290C
;
; CURRENT APPLICATION NUMBER: US/10/092
; CURRENT FILING DATE: 2002-03-07
;
; PRIOR APPLICATION NUMBER: USSN 60/200400
; PRIOR FILING DATE: 2001-03-08
;
; PRIOR APPLICATION NUMBER: USSN 60/200400
; PRIOR FILING DATE: 2001-04-13
;
; PRIOR APPLICATION NUMBER: USSN 60/300400
; PRIOR FILING DATE: 2001-04-13
;

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;; PRIOR FILING DATE: 2001-12-03
;; PRIOR APPLICATION NUMBER: US 60/274,281
;; PRIOR FILING DATE: 2001-03-08
;; PRIOR APPLICATION NUMBER: US 60/274,191
;; PRIOR FILING DATE: 2001-03-08
;; PRIOR APPLICATION NUMBER: US 60/325,681
;; PRIOR FILING DATE: 2001-09-27
;; PRIOR APPLICATION NUMBER: US 60/304,354
;; PRIOR FILING DATE: 2001-07-10
;; PRIOR APPLICATION NUMBER: US 60/279,995
;; PRIOR FILING DATE: 2001-03-30
;; PRIOR APPLICATION NUMBER: US 60/294,899
;; PRIOR FILING DATE: 2001-05-31
;; PRIOR APPLICATION NUMBER: US 60/287,424
;; PRIOR FILING DATE: 2001-04-30
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 768
SEQ ID NO 81
LENGTH: 4268
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(4258)
US-10-092-900A-81

Query Match 67.1%; Score 1231.8; DB 17; Length 4268;
Best Local Similarity 86.1%; Pred. No. 0;
Matches 1535; Conservative 0; Mismatches 37; Indels 211; Gaps 7;
Qy 1 CTGAGCCAACTTTGTTGACCATCTCGCAATGCTTGGAGCTCTGTCATAGAGACTTT 60
Db 2516 CTGAGCCAACTTTGTTGACCATCTCGCAATGCTTGGAGCTCTGTCATAGAG- 2569
Qy 61 TCCCTTAGTGGCCAGAGTCTGCTCAACCTGCTGGAATCTTCAACCCCACTATATGC 120
Db 2570 -----AGGTGCCAGAGTCTGCTCAACCTGCTGGAATCTTCTGAACCCCACTATATGC 2623
Qy 121 GGCAAGTGTCTCTGGGAAACCCAGACAAGTCCCAAGTGCAGCAGG----- 165
Db 2624 GGCAAGTGTCTCTGGGAAACCCAGACAAGTCCCAAGTGCAGCAGGCGGTTTGTGTA 2683
Qy 166 ----- 165
Db 2684 ACTCGTTCTGACCTCTCGGAGAACTCCCAAGAGTAGCCAGGCTGGAGGCTTCAGCC 2743
Qy 166 -----CCAGCAGCATGCGCAGCTGCTGGTGGGTGAGCGGTATGACACGAGG 218
Db 2744 GAGCCTACAGAGCAGCATGCGCAGCTGCTGGGTGAGCGGTATGACACGAGG 2803
Qy 219 ACTTCTCTGTGGTCTGAGCCCTTCTTCCAGAACATCCAGCTCCCTGTCTG----- 271
Db 2804 ACTTCTCTGTGGTCTGAGCCCTTCTTCCAGAACATCCAGCTCCCTGTCTGAGGATG 2863
Qy 272 ----- 271
Db 2864 GGCTCCAGATACGCTCTTTTGGCCAGACTGCATCCACCCAAATCAGAAATTCACACT 2923
Qy 272 -----GGCTTGAACCACTTTGGAAGCAAAACAGAGA 302
Db 2924 CCCAGCTGGCAGAGCCCTTTGGACCAATATGCTTGAACCACTTTGGAAGCAAAACAGAGA 2983
Qy 303 CCCTGGACCTGAGAGCAGAGATGCCCATCACTGTCCCACTCAGAATGAGCCCTTCCTGA 362
Db 2984 CCCTGGACCTGAGAGCAGAGATGCCCATCACTGTCCCACTCAGAATGAGCCCTTCCTGA 3043
Qy 363 GAACCCCTCGGAATAGTAATACAGTACCGTACCCTATCAAGCCAGCCATTTGAGAACTGGGCA 422
Db 3044 GAACCCCTCGGAATAGTAATACAGTACCGTACCCTATCAAGCCAGCCATTTGAGAACTGGGCA 3103
Qy 423 GTGACTTCTGTGTACAGAGTGGAGGCTTCCATAGTGTCCAACTCTGTCCACAGC 482
Db 3104 GTGACTTCTGTGTACAGAGTGGAGGCTTCCATAGTGTTCCAACCTCTGTCCACAGC 3163

Qy 483 TCCGACCAGCAGACATCAAAAGTGGTGGCCCGCTGGGTGACTCTCTGACTACAGCAGTGG 542
Db 3164 TCCGACCAGCAGACATCAAAAGTGGTGGCCCGCTGGGTGACTCTCTGACTACAGCAGTGG 3223
Qy 543 GAGCTCGACCAAACTCAAGTGAACCTACCAATCTTGGAGGGGACTCTCTTGGAGCA 602
Db 3224 GAGCTCGACCAAACTCAAGTGAACCTACCAATCTTGGAGGGGACTCTCTTGGAGCA 3283
Qy 603 TTGGAGGGGATGGAACTTTGGAGACTCACACACACTGCCAACTTCTGAAGAAGTTCA 662
Db 3284 TTGGAGGGGATGGAACTTTGGAGACTCACACACACTGCCAACTTCTGAAGAAGTTCA 3343
Qy 663 ACCCTTACCTCTCTTGGCTTCTTACCAAGCACCCTGGAGGGGACAGCAGGACTAAATGTGG 722
Db 3344 ACCCTTACCTCTCTTGGCTTCTTACCAAGCACCCTGGAGGGGACAGCAGGACTAAATGTGG 3403
Qy 723 CAGCGGAAGGGCCAGAGCT---AGGACATATGCCAGCCAGCCCTGGGACTCTGTAGAGC 779
Db 3404 CAGCGGAAGGGCCAGAGCTTAGGAGGACATGCCAGCCAGCCCTGGGACTCTGTAGAGC 3463
Qy 780 GAATGAAAAACAGCCCGACATCAACCTGGAGAAAGACTGGAAGCTGTCACACTTCA 839
Db 3464 GAATGAAAAACAGCCC---CATACACTTTCAGGAAGACTGGAAGATAATAACCTCTGTTA 3520
Qy 840 TTGGGGTCAACGACTTGTGTCTTACTGTGAGAAATCCGAGAGGCCCACTTGGCCACGGAAT 899
Db 3521 TAGCGGCAATGACCTCTGTGATTTCTGCAATGATC-----TGTAGGTGAAT 3568
Qy 900 ATGTTTACGACATCAACAGGCCCTTGAACATCTCTCTGAGGAGCTCCCAAGGGCTTTG 959
Db 3569 ATGTTTACGACATCAACAGGCCCTTGAACATCTCTCTGAGGAGCTCCCAAGGGCTTTG 3628
Qy 960 TCAACGTGTGGAGGTCTATGAGTGGCTAGCTGTACAGGGGCAAGGGGGAAATGTG 1019
Db 3629 TCAACGTGTGTGGAGGTCTATGAGTGGCTAGCTGTACAGGGGCAAGGGGGAAATGTG 3688
Qy 1020 CCATGTGTGGAGCTCAGAACAACTTGCACTTGGCTCAGACACTCGCAAGCTCCCTGGAGA 1079
Db 3689 CCATGTGTGGAGCTCAGAACAACTTGCACTTGGCTCAGACACTCGCAAGCTCCCTGGAGA 3748
Qy 1080 AGCAAGAACTGAAGAAAGTGAACCTTCAGCATGGCATCTCAGTTTCTCTACT 1139
Db 3749 AGCAAGAACTGAAGAAAGTGAACCTTCAGCATGGCATCTCAGTTTCTCTACT 3808
Qy 1140 GGCAACCAATACACACGCTGAGGACTTTGCGGTGTGTGTCAGCTTCTTCCAAACA 1199
Db 3809 GGCAACCAATACACACGCTGAGGACTTTGCGGTGTGTGTCAGCTTCTTCCAAACA 3868
Qy 1200 CACTCACCCCACTGAACGAGAGAGGGGACACTGACCTTCACTTCTTCTCGAGGACTGTT 1259
Db 3869 CACTCACCCCACTGAAC---AGAGGGGACACTGACCTCACTTCTTCTCGAGGACTGTT 3925
Qy 1260 TTCACTTCTCAGACCGGGGCATGCCAGATGGCCATCTGCACTCTGGAACAAATGCTGG 1319
Db 3926 TTCACTTCTCAGACCGGGGCATGCCAGATGGCCATCTGCACTCTGGAACAAATGCTGG 3985
Qy 1320 AACCACTGGGCGCAGAGTACCTCCAACTTCCACCAAGCTTCCACAGCCAGCCAACTCAAGT 1379
Db 3986 AACCACTGGGCGCAGAGTACCTCCAACTTCCACCAAGCTTCCACAGCCAGCCAACTCAAGT 4045
Qy 1380 GCCCTCTCTCTGAGAGCCCTTACTCTTACACCTTGGCGAAACAGCCGATGCTCCAGACC 1439
Db 4046 GCCCTCTCTCTGAGTCTTACTCTTACACCTTGGCGAAACAGCCGATGCTCCAGACC 4105
Qy 1440 AGGTGAAGAAGCCCGAGGTGCTTACTTGGGTGTCTCCAGTGGGAGCGGAGTCTGGCC 1499
Db 4106 AGGTGAAGAAGCCCGAGGTGCTTACTTGGGTGTCTCCAGTGGGAGCGGAGTCTGGCC 4165
Qy 1500 TTGTGTGGGATCATCGGACAGTGTCTTGGAGGTGTCAGGAGGTGGCGGAGGAGAG 1559
Db 4166 TTGTGTGGGATCATCGGACAGTGTCTTGGAGGTGTCAGGAGGTGGCGGAGGAGAG 4225

1560 ATCTCTCAAATGAGCTGTGGCCACTGTGGCCCTCTAGGCCCGGG 1602
|||||
4225 ATCTCTCAAATGAGCTGTGGCCACTGTGGCCCTCTAGGCCCGGG 4268
|||||

```

RESULT 6
US-10-276-774-73
, Sequence 73, Application US/10276774
, Publication No. US20040053245A1
, GENERAL INFORMATION:
, APPLICANT: Hyseq, Inc.
, APPLICANT: Tang, Y, Tom et al
, TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
, FILE REFERENCE: 21272-030
, CURRENT APPLICATION NUMBER: US/10/276, 774
, CURRENT FILING DATE: 2002-11-18
, PRIOR APPLICATION NUMBER: 09/560, 875
, PRIOR FILING DATE: 2000-04-27
, PRIOR APPLICATION NUMBER: 09/496, 914
, PRIOR FILING DATE: 2000-02-03
, NUMBER OF SEQ ID NOS: 2700
, SOFTWARE: Cuscom
, SEQ ID NO 73
, LENGTH: 802
, TYPE: DNA
, ORGANISM: Homo sapiens
US-10-276-774-73

```

Query Match	36.4%	Score	667.4	DB	17	Length	802
Best Local Similarity	99.9%	Pred. No.	3.7e-170	Indels	0	Gaps	0
Matches	668	Conservative	0	Mismatches	1		
274	GCTTGAAACACATTGGAAAGCAAACACAGACACCCCTGGACCTGAGAGCAGAGATGCCATCAC	333					
134	GCTTGAAACACATTGGAAAGCAAACACAGACACCCCTGGACCTGAGAGCAGAGATGCCATCAC	193					
334	CTGTCACCATCAGAAATGAGCCCTTCTGAGAACCCCTCGGAATAGTAATACACAGCTACCC	393					
194	CTGTCACCATCAGAAATGAGCCCTTCTGAGAACCCCTCGGAATAGTAATACACAGCTACCC	253					
394	CATCAAGCCAGCCATTGAGAACTGGGGCAGTGACTTCTGTGTACAGATGGAAAGGCTTC	453					
254	CATCAAGCCAGCCATTGAGAACTGGGGCAGTGACTTCTGTGTACAGATGGAAAGGCTTC	313					
454	CAATAGTGTTCAAACCTCTGTCCACAGCTCCGACACAGACATCAAAGTGTGTGGCCGC	513					
314	CAATAGTGTTCAAACCTCTGTCCACAGCTCCGACACAGACATCAAAGTGTGTGGCCGC	373					
514	CCTGGGTGACTCTCTGACTACAGCAGTGGGAGCTTGAACCAACATCTCCAGTGACCTACC	573					
374	CCTGGGTGACTCTCTGACTACAGCAGTGGGAGCTTGAACCAACATCTCCAGTGACCTACC	433					
574	CACATCTTTGGAGGGGACCTCTCTTGGAGCATTTGGAGGGGATGGGAATCTTGGAGACTCAC	633					
434	CACATCTTTGGAGGGGACCTCTCTTGGAGCATTTGGAGGGGATGGGAATCTTGGAGACTCAC	493					
634	CACATGCCCCAACATTCTGAAGAAATTCACCCCTTACCTCTTGGCTCTCTTACACAGAC	693					
494	CACATGCCCCAACATTCTGAAGAAATTCACCCCTTACCTCTTGGCTCTCTTACACAGAC	553					
694	CTGGAGGGGACAGCAGAGACTTAATGTGGCAGGGGAAGGGGCCAGAGCTAGGGACATGCC	753					
554	CTGGAGGGGACAGCAGAGACTTAATGTGGCAGGGGAAGGGGCCAGAGCTAGGGACATGCC	613					
754	AGCCAGGCTGGGACCTGGTAGACGATGAAACACAGCCCCCGACATCAACTGGAGAA	813					
614	AGCCAGGCTGGGACCTGGTAGACGATGAAACACAGCCCCCGACATCAACTGGAGAA	673					
814	AGACTGGAGCTGTGTACACACTCTTCATTTGGGGTCAACGATTTGTGCTATTACTGTGAGAA	873					
674	AGACTGGAGCTGTGTACACACTCTTCATTTGGGGTCAACGATTTGTGCTATTACTGTGAGAA	733					

```

|||||
734 TCCGAGGCCCACTTGGCCACGGGAATATTGTTCAGCACATCCAACAGGCCCTGGACATCCT 793
|||||
934 CTCTGAGGA 942
|||||
794 CTCTGAGGA 802
Db

RESULT 7
US-10-296-115-600
; Sequence 600, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 600
; LENGTH: 802
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-600
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Query Match	36.4%	Score 667.4	DB 17	Length 802
Best Local Similarity	99.9%	Pred. No. 3.7e-170		
Matches 668	Conservative 0	Mismatches 1	Indels 0	Gaps 0
274	GC	TTGAACCACTTTGGAACCAAAA	CAGAGACCTCTGGACCTGAGACGAGAGATGCCATCAC	333
134	GC	TTGAACCACTTTGGAACCAAAA	CAGAGACCTCTGGACCTGAGACGAGAGATGCCATCAC	193
334	CT	GTCCCACTCAGATGAGCCCTTCT	TGAGAAACCCCTCGGAATAGTAACTPACAGTACCC	393
194	CT	GTCCCACTCAGATGAGCCCTTCT	TGAGAAACCCCTCGGAATAGTAACTPACAGTACCC	253
394	CAT	CAAGCCAGCGCATTTGAGAACT	TGGGGCAGTGAATCTCTGTGTACAGATGGAAGGCTTC	453
254	CAT	CAAGCCAGCGCATTTGAGAACT	TGGGGCAGTGAATCTCTGTGTACAGATGGAAGGCTTC	313
454	CAT	ATAGTGTTCCAAACCTCTGT	CCACAGCTCCGACCAGACACATCAAAAGTGTGGCCGC	513
314	CAT	ATAGTGTTCCAAACCTCTGT	CCACAGCTCCGACCAGACACATCAAAAGTGTGGCCGC	373
514	CCT	GGGTGATCTCTGACTACAGAGT	GGGAGCTCGACCAAAACAATCTCAGTGAACCTTACC	573
374	CCT	GGGTGATCTCTGACTACAGAGT	GGGAGCTCGACCAAAACAATCTCAGTGAACCTTACC	433
574	CAC	ATCTTTGGAGGGGAGCTCTCT	TTGGAGCATTTGGAGGGATGGGACCTTGGAGACTCAAC	633
434	CAC	ATCTTTGGAGGGGAGCTCTCT	TTGGAGCATTTGGAGGGATGGGACCTTGGAGACTCAAC	493
634	CAC	ACTGCCCAACATTCGTAAGAAG	TTCAAACCTTACCTCTCTTGGCTTCTCTACAGAC	693
494	CAC	ACTGCCCAACATTCGTAAGAAG	TTCAAACCTTACCTCTCTTGGCTTCTCTACAGAC	553
694	CT	GGAGGGGACAGCAGGACTAAAT	TGTGGCAGCGGAGGGCCAGAGCTTAGGGACATGCC	753
554	CT	GGAGGGGACAGCAGGACTAAAT	TGTGGCAGCGGAGGGCCAGAGCTTAGGGACATGCC	613
754	AG	CCACAGCGCTGGGACCTTGGT	TAGACGAATGAAAAACGCCCGACATCAACCTGGAGAA	813
614	AG	CCACAGCGCTGGGACCTTGGT	TAGACGAATGAAAAACGCCCGACATCAACCTGGAGAA	673
814	AGA	CTGGAAGTGTGTTACACTTCTAT	TGGGGTCAACGACTTGTGTCACTTACTGTGTGAGAA	873
674	AGA	CTGGAAGTGTGTTACACTTCTAT	TGGGGTCAACGACTTGTGTCACTTACTGTGTGAGAA	733

Qy 874 TCCGAGGCGCCACTTGGCCACGGGAATATGTTTCAGACATCCAAACAGGCGCTGGACATCCT 933
 Db 734 TCCGAGGCGCCACTTGGCCACGGGAATATGTTTCAGACATCCAAACAGGCGCTGGACATCCT 793
 Qy 934 CTCTGAGGA 942
 Db 794 CTCTGAGGA 802

RESULT 8
 US-10-264-237-323
 ; Sequence 323, Application US/10264237
 ; Publication No. US2004009491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birse et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PAL31P1
 ; CURRENT APPLICATION NUMBER: US/10/264,237
 ; CURRENT FILING DATE: 2002-10-04
 ; PRIOR APPLICATION NUMBER: PCT/US01/16450
 ; PRIOR FILING DATE: 2001-05-18
 ; PRIOR APPLICATION NUMBER: US 60/205,515
 ; PRIOR FILING DATE: 2000-05-19
 ; NUMBER OF SEQ ID NOS: 2876
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO 323
 ; LENGTH: 861
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (802)..(802)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (846)..(846)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; US-10-264-237-323

Query Match 31.3%; Score 575; DB 17; Length 861;
 Best Local Similarity 99.1%; Pred. No. 4.2e-145;
 Matches 578; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1218 AGAGAGGACACTGACCTACCTCTTCTCCGAGGACTGTTTTCACTTCTCAGACCGCG 1277
 Db 1 AGAGAGGACACTGACCTACCTCTTCTCCGAGGACTGTTTTCACTTCTCAGACCGCG 60

Qy 1278 GGCATGCCGAGATGGCCATCGCACTCTGGAAACAATGCTGGAAACCAAGTGGGCGCGAAGA 1337
 Db 61 GGCATGCCGAGATGGCCATCGCACTCTGGAAACAATGCTGGAAACCAAGTGGGCGCGAAGA 120

Qy 1338 CTACCTCCAAACAATTACCCACAGCGAGCAAACTCAAGTGCCTCTCTCTCAGAGGCC 1397
 Db 121 CTACCTCCAAACAATTACCCACAGCGAGCAAACTCAAGTGCCTCTCTCTCAGAGGCC 180

Qy 1398 CTTACCTCTACACCTTCGGAAACAGCGGATGCTCCAGACAGGCTGAAGAACCCCGC 1457
 Db 181 CTTACCTCTACACCTTCGGAAACAGCGGATGCTCCAGACAGGCTGAAGAACCCCGC 240

Qy 1458 AGGTGCTCTACTGGCTGTCCAGTGGCAGCGGAGTGGGCTTGTGGTGGGCATCATCG 1517
 Db 241 AGGTGCTCTACTGGCTGTCCAGTGGCAGCGGAGTGGGCTTGTGGTGGGCATCATCG 300

Qy 1518 GGACAGTGGTCTGGAGGTGAGGAGAGTGGCGCGAGGAGATCCCTCAATGAGCCTGC 1577
 Db 301 GGACAGTGGTCTGGAGGTGAGGAGAGTGGCGCGAGGAGATCCCTCAATGAGCCTGC 360

Qy 1578 GCATGTGGCCCTCTAGGCGCGGGGTGGGTCTCACCCTAAATCCCTATAGCACTCT 1637
 Db 361 GCATGTGGCCCTCTAGGCGCGGGGTGGGTCTCACCCTAAATCCCTATAGCACTCT 420

Qy 1638 CTTACCGCCTCTGCGCCCGAGCCACTCCGCGCCACAGGACATGCTTCAATGCTGTGTC 1697

Db 421 CTTCACTGCCCTCTGCCCCAGCCACTCCCGGCCACACAGGACATGCTTCAATGCTGTGTC 480
 Qy 1698 CATAGGAAGCCCGAGGGACAGTCAAACTTCTTGGGGCCTGGGCTTCTTCCAGGCTATG 1757
 Db 481 CATAGGAAGCCCGAGGGACAGTCAAACTTCTTGGGGCCTGGGCTTCTTCCAGGCTATG 540
 Qy 1758 CTCTGGAATGGATACATATTAAATAAAGTCCAAAGCTATTATTA 1800
 Db 541 CTCTGGAATGGATACATATTAAATAAAGTCCAAAGCTATTATTA 583

RESULT 9
 US-09-764-891-1391
 ; Sequence 1391, Application US/09764891
 ; Publication No. US20030077808A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC006
 ; CURRENT APPLICATION NUMBER: US/09/764,891
 ; CURRENT FILING DATE: 2001-01-17
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 10231
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1391
 ; LENGTH: 572
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (375)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: SITE
 ; LOCATION: (529)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; US-09-764-891-1391

Query Match 21.6%; Score 396.2; DB 10; Length 572;
 Best Local Similarity 96.6%; Pred. No. 1e-96;
 Matches 477; Conservative 2; Mismatches 6; Indels 9; Gaps 7;

Qy 274 GCTTGAACCACTTGGGAAGCAAAACAGAGACCTCGGACCTGAGACAGAGATGCCCATCAC 333
 Db 30 GCTTGAACCACTTGGGAAGCAAAACAGAGACCTCGGACCTGAGACAGAGATGCCCATCAC 89

Qy 334 CTGTCCCACTCAGAACTGAGCCCTTCTGAGAACCCCTCGGAATAGTAACACGTACCC 393
 Db 90 CTGTCCCACTCAGAACTGAGCCCTTCTGAGAACCCCTCGGAATAGTAACACGTACCC 149

Qy 394 CATCAAGCCAGCCATTGAGAACTGGGGCAGTGACTTCTGTGTACAGAGTGGAGGCTTC 453
 Db 150 CATCAAGCCAGCCATTGAGAACTGGGGCAGTGACTTCTGTGTACAGAGTGGAGGCTTC 209

Qy 454 CAATAGTGTTCACACCTCTGTCCACAGCTCCGACAGCAGACATCAAGTGTGGCGGC 513
 Db 210 CAATAGTGTTCACACCTCTGTCCACAGCTCCGACAGCAGACATCAAGTGTGGCGGC 269

Qy 514 CTTGGGTGACTCTCTGACTACAGCAGTGGGAGCTTCGACCAAAACAACTCCAGTG-ACCTAC 572
 Db 270 CTTGGGTGACTCTCTGACTACAGCAGTGGGAGCTTCGACCAAAACAACTCCAGTG-ACCTAC 329

Qy 573 CCACATCTTGGAGGGGACTCTCTT-GGAGCATTTGGAGGGATGGGAA--CTTGGAGACTC 629
 Db 330 CCACATCTTGGAGGGGACTCTCTTGGAGCATTTGGAGGGATGGGAACTTGGAGACTC 389

Qy 630 ACACCACTGCGCCCAACATTTCTGAAGAAGTTCAACCTTACCTCTTGGGCTTCT-ACC 688
 Db 390 ACACCACTGCGCCCAACATTTCTGAAGAAGTTCAACCTTACCTCTTGGGCTTCTTCTGACC 449

Qy 689 AGCAGCTGGG--AGGGGACAGAGGACT-AAATGTGCGAGCGGAAGGGCCAGAGCTA-G 744
 Db 450 AGCAGCTGGGAGGGGAGCAGAGGACTGAAATGTGCGAGCGGAAGGGCCAGAGTAGG 509

Mon Mar 28 09:43:24 2005

QY 745 GGACATGCCAGCC 758
Db 510 GGACATGCCAGCC 523

RESULT 10
US-10-092-900A-83
; Sequence 83, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zehrusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha T.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Hailong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 83
; LENGTH: 1624
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

LOCATION: (311)..(1241)
US-10-092-900A-83

Query Match 11.5%; Score 210.6; DB 17; Length 1624;
Best Local Similarity 55.1%; Pred. No. 3.3e-46; Indels 27; Gaps 3;
Matches 492; Conservative 0; Mismatches 374;

QY 488 CCAGCAGACATCAAAAGTGGTGGCGCCCTGGTGACTCTCTGACTACAGCAGTGGAGCT 547
Db 2 CCGGCTGACATCAATGTAATTGGAGCCCTGGTGACTCTCTCAGCGCAGCAATGGGGCC 61

QY 548 CG-----ACCAACAACTCCAGTGACTCCACATCTTGGAGGGGACTCTTTGGAGC 601
Db 62 GGGTCCACACCTGGGAACGCTTTGGACGCTTTGACTCAGTACCGAGGCCCTGCTCTGGAGC 121

QY 602 ATTGAGGGGATGGAACTTTGGAGACTCACACACACTGCCCAACATTTCTGAAAGATTTC 661
Db 122 GTCGGCGGAGATGAGAACATCGGCACCGTGTACCCCTGGCGAACATCTCTCCGGGAATTC 181

QY 662 AACCTTTACCTCTTTGGCTTTCTTACACAGCACCTGGGAGGGGAC-----AGCAGGA 712
Db 182 AACCTTTCTCTGAAGGGCTTTCTTGTGGCACTGGGAAAGAACAGTCTTAATGCTTC 241

QY 713 CTAATGTGGCAGCGAAGGGCGAGAGCTAGGGACATGCCAGCCAGGCCCTGGGAGCTG 772
Db 242 TTAACACAGGCTGTGGCGAGGAGGCCGAGCTGAGGATCTACCTGTCCAGGCCAGGAGGCTG 301

QY 773 GTAGAGCGAATGAAACACAGCCCCGACATCACTGGAGAGAGACTGGAAGCTGTGTACA 832
Db 302 GTGACCTGATGAAGATGACACAGGATACATTTTCAGGAAGACTGGGAAGATATATACC 361

QY 833 CTCTTCATTTGGGTCAACGACTTGTCTCATTAATCTGTGAGAAATCCGGAGGCCCATCTGGCC 892
Db 362 CTGTTTATAGGCGCAATGACCTCTGTGATTTCTGCAATGATCTGTCTCACTATTCTCCC 421

QY 893 ACGGAATATGTTACAGCACATCCAAACAGGCCCTGGACATCTCTCTGAGAGCTTCCCAAGG 952
Db 422 CAGAACTTCACAGACAACTTTGGAAGGCCCTGGACATCTCTCATGTGAGGTTCTTCGG 481

QY 953 GCTTTCGTCACAGTGGTGGAGGTCATGAGCTGGCTAGCTGTACCCAGGCGCCAAAGCGGG 1012
Db 482 GCATTTGTGAACCTGGTGACGGTCTTGAGATCGTCAACCTGAGGGAGCTGTACCAGGAG 541

QY 1013 AATGTGCGCATGCTGGCAGCTCAGAACAACTGCACTTG-----CCTCAGACAC 1060
Db 542 AAAAAGTCTACTGCCCCAAGGATGATCTCAGGTTCTGTGTCTCTGTCTCTGAGTTT 601

QY 1061 TCGCAAGCTCCTCGAGAGACAGAACTGAAAGAAAGTGAACCTGGAACCTCCAGCATGGC 1120
Db 602 GATGATACTCAACAGAACTTGTACCTCTGATGATGATGATGATGATGATGATGATGATG 661

QY 1121 ATCTCCAGTTTCTCTCTACTGCGACCAATACACACAGCGTGGAGGCTTTCGGTTGTGTG 1180
Db 662 ACCACCAACTGATTCAGAGTGGCGGATATGACACAGGGGAAGATTTTACTGTGTGTGTG 721

QY 1181 CAGCCTTTTTCAAAAACACACTCACCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1240
Db 722 CAGCGGTTTCTTTGAAAAACGTTGACATGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 781

QY 1241 TTCTTCTCGAGGACTGTTTTCATCTTCTCAGACCGCGGGCATGCCAGATGCCATCCCA 1300
Db 782 TTCTTCTCGTCTGACTGTTTTCATCTTCTCAGCAGCAGTCTCTCACTCCCGAGAGACCCAGTGT 841

QY 1301 CTCTGGAACCAACTGTCTGGACAGTGGCGCGGCGGCAAGACTACCTCCCAACAACTT 1353
Db 842 CTCTGGAACCAATATGCTGGAGCCTGTGTGGCCAGAACGACTCGTCTCATAGTT 894

RESULT 11
US-10-094-749-390
; Sequence 390, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOTYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094.749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 390
LENGTH: 2477
TYPE: DNA
ORGANISM: Homo sapiens
US-10-094-749-390

Query Match 10.2%; Score 186.8; DB 17; Length 2477;
Best Local Similarity 54.7%; Pred. No. 1.1e-39;
Matches 427; Conservative 0; Mismatches 332; Indels 21; Gaps 2;
595 TTGAGCATTGGAGGGATGGAACTTTGGAGACTCACACCACTGCCCACATCTTCTGAA 654
Db |||||
2 TTACAGCGTGGCGGAGATGAGACATCGGCACCGTTTACCACTTGGCGACATCTCTCG 61
555 GAAGTTCAACCTTACCTCTTGGCTTCTTACAGACACTGGAGGGGACA----- 706
Db |||||
62 GGAATTCACCCCTTCCCTTGAAGGGCTTCTGTGGCAGCTGGGAAAGAACCACTCTAA 121
Qy |||||
707 -GCAGGACTAATGTGGCAGCGGAGGGCCAGAGCTAGGACATGCCAGCCAGGCTG 765
Db |||||
122 TGCCTCTTAAACAGCGCTGTGGCAGGAGGCGGAGCTGAGGATCTTACCTGTCCAGGCCAG 181
Qy |||||
766 GGACCTGTAGAGCGAATGAAACAGCCCGACATCAACCTGGAGAAAGACTGGAAGCT 825
Db |||||
182 GAGCTGTGGACCTGATGAGATGACACGAGGATACATTTTCCAGGAGACTGGAAGAT 241
Qy |||||
826 GGTCAACTCTTCAATGGGGTCAACGACTTGTGCTATCTGTGAGAAATCCGAGGCCA 885
Db |||||
242 AATAACCCCTGTTATAGCGCGCAATGACCTGTGTGATTTCTGCAATGATCTGTGCCACTA 301
Qy |||||
886 CTTGGCCACGGAATATGTTACAGACATCCACAGCCCTGGACATCTCTCTGAGGAGCT 945
Db |||||
302 TTCTCCCGAAGCTTTCACAGACAATTTGGAAGAGCCCTGGACATCTCTTCCATGCTGAGGT 361
Qy |||||
946 CCCAAGGCTTTCGTCAACGTGGTGGAGGTCTATGGAGCTGGCTAGCTGTACCAAGGCCA 1005
Db |||||
362 TCCTCGGCAATTTGTGAACCTGGTGAACGCTGCTTGGATCTCAACCTGAGGAGCTGTA 421
Qy |||||
1006 AGCGGGGAATGTGCCATGTGGCAGCTCAGAAACAATGCACTTG-----CCT 1053
Db |||||
422 CCAGGAGAAAAAGTCTACTGCCCAAGGATGATCTCAGGTCTCTGTGTCTCTGTCTCT 481
Qy |||||
1054 CAGACACTCGGAAGCTCCCTGGAGAGCAGACACTGAGAAAGTGAACCTGGAACCTCCA 1113
Db |||||
482 GAAGTTGATGATAACTCAACAGAACTTGTACCTCTCATCGAATTCACAGAAAGTTTCA 541

Qy 1114 GCATGGCATCTCCAGTTTCTCTACTGSCACCAATACACACGGTGTGAGGACTTTTGCCT 1173
Db |||||
542 GGAGAAGACCCACCAACTGATTGAGAGTGGGCGATATGACACAAGGGAAGATTTTACTGT 601
Qy 1174 TGTGTTGAGGCTTTCTTCCAAACACACTCACCCCACTGAAACGAGAGAGGGGACACTGA 1233
Db |||||
602 GGTGTGAGCGGTTCTTTGAAAAACGTGGACATGCCAAAGACCTCGGAAGGATTTGCCTGA 661
Qy 1234 CCTCACCTTCTTCTCCGAGGACTGTTTTTCACTTCTCAGACCGCGGGGATGCCGAGATGCG 1293
Db |||||
662 CAACTCTTTCTTCTGCTCTGACTGTTTCCACTTTCAGCAGCAAGTCTCTCTCCGAGCAGC 721
Qy 1294 CATGCACTCTGGAACCAACATGCTGGAACCAAGTGGCGGCGCAAGTACTCTTCAACAACTT 1353
Db |||||
722 CAGTGCTCTCTGGAACAATATGCTGGAGCCTGTTTGGCCAGAGACGACTCGTCTATAAGTT 781
RESULT 12
US-10-276-774-257
; Sequence 257, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 257
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-257

Query Match 5.0%; Score 91; DB 17; Length 399;
Best Local Similarity 59.1%; Pred. No. 4.4e-14;
Matches 179; Conservative 0; Mismatches 115; Indels 9; Gaps 1;
565 TGACCTACCCACATCTTTGGAGGGGACTCTCTTGAGCATTTGGAGGGATGGGAACTTGA 624
Db |||||
97 TAACCTTTCAATTTTCTTTTGGACCCACGTTACAGCGTCGCGGAGATGAAACATCGG 156
Qy |||||
625 GACTCACACCACTGCCCACATTTCTGAAGAAGTTTCAACCTTTACCTCTTGGCTTCTC 684
Db |||||
157 CACGTTTACCACTTGGCGAATCTCTCCGGAATTCACCTTCCCTGAAGGCTTCTC 216
Qy |||||
685 TACCAGACCTGGAGGGGACA-----GCAGGACTAAATGTGGCAGCGGAGGGGC 735
Db |||||
217 TGTGGCAGCTGGGAAAGAAACCAAGTCTTAATGCTTCTTAAACCAAGGCTGTGGCAGG 276
Qy |||||
736 CAGAGCTAGGAGCATGCCAGCGCTGGACCTGTAGAGCGAATGAAAAACAGCC 795
Db |||||
277 CCAGCTGAGGATCTTACCTGTCCAGGCCAGAGGCTGTGAGCTGTATGAAGATGACAC 336
Qy |||||
796 CGACATCAACCTCGAGAAAGACTGGAAAGCTGGTGCACACTCTTCAATTGGGGTCAACGACTT 855
Db |||||
337 GAGGATACACTTTCAGGAAGACTGGAGATAATAACCTCTGTATAGCGCAATGACCT 396
Qy |||||
856 GTG 858
Db |||||
397 CTG 399

RESULT 13
US-10-357-930-52986/c
; Sequence 52986, Application US/10357930

1741 CTTCTTCAGGCTATGCTCCTGGAATGATACATTTAAATAAAGTCCAAAGCTATTTTA 1800
172 CTTTAAACCTTTTAAACCCCAATGGGTATTTTATCCAAATCCAGTTTATTTTA 113
1801 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1835
112 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 78

RESULT 15
US-10-723-860-3816
; Sequence 3816, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods for Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3816
; LENGTH: 298
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (254)..(255)
; OTHER INFORMATION: n is a, c, g, or t
US-10-723-860-3816

Query Match 3.1%; Score 56.2; DB 18; Length 298;
Best Local Similarity 52.9%; Pred. No. 0.0001;
Matches 118; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

1613 ACCCTAAACTCCCTATAGCCACTCTCTTACCGCCCTCTGCCCCAGCCACTCCCGGCAC 1672
69 ACCGTAAACAAACACGCCCCCTCCCTTCCAGCCCTGAGCGGGAACATCTCCAGGAC 128
1673 CAGGACATGCTTCATGCTGTCGATAGGTCATAGGAGCCAGGAGGACAGTCACTTCTTGG 1732
129 CTTGCCCTGCTCACCTATGTTGTCACCTATCTCTCTGCGCTTTTCAAGTCTTTG 188
1733 GGCCTGGGCTTCTTCCAGGCTTATGCTCTGGAATGGATACATTTAAATAAAGTCCAAAG 1792
189 GCTGTGACTTTTCATCTCTGCTCTTTAGTCTAAAAATAAATACTGGAGATAAAAAA 248
1793 CTATTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1835
249 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 291

Search completed: March 27, 2005, 12:54:56
Job time : 1074.69 secs

Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52986
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-52986

Query Match 4.6%; Score 83.8; DB 18; Length 393;
Best Local Similarity 88.3%; Pred. No. 3.9e-12;
Matches 91; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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198 GACATCAACCTCGAGAAAGCTGGAAGCTGTGCACACTTTCATTTGGGTCAACGACTTG 139
857 TGTCATTACTGTGGAATCCGAGGCCACCTTGGCCACGGAAT 899
138 TGTCATTACTGTGGAATCCGAGGCCACCTTGGCCACGGAAT 96

RESULT 14
US-10-425-115-126452/c
; Sequence 126452, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 126452
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_46792C.1
US-10-425-115-126452

Query Match 3.1%; Score 56.6; DB 18; Length 568;
Best Local Similarity 74.7%; Pred. No. 0.00011;
Matches 71; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 13:10:00 ; Search time 5913.96 Seconds
(without alignments)
11810.698 Million cell updates/sec

Title: US-09-778-961-1
Perfect score: 1835
Sequence: 1 ctgcagccaactttgtgac.....aaaaaaaaaaaaaaaaaa 1835

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gse1.*
9: gb_gse2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1443	78.6	1661	3	CR612785
2	1081	58.9	1561	3	CR600701
3	866.8	47.2	870	1	AL542856
4	768.4	41.9	935	5	BU150503
5	760.6	41.4	903	5	EX349938
6	729.2	39.7	925	5	EX349937
7	697.6	38.0	822	5	EX369782
8	677.4	36.9	1033	4	BM549919
9	628	34.2	716	5	BU683311
10	627.8	34.2	823	4	BU488437
11	624	34.0	625	6	CA447656
12	607	33.1	607	4	BM714799
13	575	31.3	583	1	AA418082
14	570.4	31.1	616	2	AA467395
15	566	30.8	567	5	BU739708
16	563.2	30.7	570	2	BF510463
17	559.8	30.5	921	5	EX354650
18	554	30.2	555	5	BU102131
19	521.4	28.4	541	2	BF854199
20	495	27.0	511	2	BE855594
21	494.6	27.0	511	2	BE645470
22	440.2	24.0	446	1	AL952246
23	435.6	23.7	685	7	CK837521
24	419.8	22.9	978	5	BU540700

25	394.2	21.5	883	4	BG697785
26	390	21.3	1081	5	BM923066
27	382	20.8	824	7	CK950790
28	365.4	19.9	587	2	AW752833
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30	359.2	19.6	458	5	EX354649
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36	321.8	17.5	827	5	EX451441
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38	310.2	16.9	701	4	BI966117
39	301.8	16.4	534	2	BE137831
40	301.4	16.4	525	2	BE684057
41	299.8	16.3	513	5	EX517602
42	296.8	16.2	763	4	BI912073
43	284.4	15.5	430	1	AA646625
44	284.4	15.5	610	7	CK955778
45	282.2	15.4	495	1	AA461827

ALIGNMENTS

RESULT 1	CR612785	1661 bp	mRNA	linear	HTC 21-JUL-2004
LOCUS	full-length cDNA clone CSODC023YA08 of Neuroblastoma Cot				
DEFINITION	25-normalized of Homo sapiens (human).				
ACCESSION	CR612785.1	GI:50493592			
VERSION	HTC: CNSLT CDNA				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue				
REFERENCE	2 (bases 1 to 1661)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr				
COMMENT	- Web : www.genoscope.cns.fr				
	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.				
FEATURES	Location/Qualifiers				
source	1..1661				
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	/clones="CSODC023YA08"				
	/tissue_type="Neuroblastoma"				
	/plasmid="pCMVSPORT_6"				
ORIGIN					
Query Match	78.6%	Score 1443;	DB 3;	Length 1661;	
Best Local Similarity	97.4%;	Pred. No. 0;			
Matches 1493;	Conservative 0;	Mismatches 40;	Gaps 1;		
Oy	274	GCTTGAACCACTTGGAGAGCAAAACAGAGACCTGGACCTGTGAGACAGATGCCATCAC	333		
Db	129	GCTTGAACCACTTGGAGAGCAAAACAGAGACCTGGACCTGTGAGACAGATGCCATCAC	188		

Qy	720	TGGCAGCGGAAAGGGCCGACGCTAGGAGCATGCGCAGCCCGCCGCTGTGGACCTGTGTAGACG	779
Db	1	TGGCAGCGGAAAGGGCCGACGCTAGGAGCATGCGCAGCCCGCCGCTGTGGACCTGTGTAGACG	60
Qy	780	GAATGAAAAACAGCCCCGACATCAACTGGAGAAAGACTGGAAGCTGGTGCACATCTTCA	839
Db	61	GAATGAAAAACAGCCCCGACATCAACTGGAGAAAGACTGGAAGCTGGTGCACATCTTCA	120
Qy	840	TTGGGGTCAACGACTTGTGTCAATTACTGTGAGAAATCCGGAGGCCACTTTGGCCACGGAAT	899
Db	121	TTGGGGTCAACGACTTGTGTCAATTACTGTGAGAAATCCGGAGGCCACTTTGGCCACGGAAT	180
Qy	900	ATGTTGAGCATCATCAACAGGCCCTTGACATCTCTCTGTGAGGAGCTCCAAAGGGCTTTGCG	959
Db	181	ATGTTGAGCATCATCAACAGGCCCTTGACATCTCTCTGTGAGGAGCTCCAAAGGGCTTTGCG	240
Qy	960	TCAAGTGTGGAGGTCAATGAGCTGTGCTAGCTGTACAGGGCCAGGGCGGGAATGTG	1019
Db	241	TCAAGTGTGGAGGTCAATGAGCTGTGCTAGCTGTACAGGGCCAGGGCGGGAATGTG	300
Qy	1020	CCATGTGGCAGCTCAGAAACAATGCACTTTGCCCTCAGACACTCGCAAGCTCCCTGGAGA	1079
Db	301	CCATGTGGCAGCTCAGAAACAATGCACTTTGCCCTCAGACACTCGCAAGCTCCCTGGAGA	360
Qy	1080	AGCAGAACTGAAGAAAGTGAATGGGAACTTCAGCATGTGGCATCTCCAGTTTCTCTACT	1139
Db	361	AGCAGAACTGAAGAAAGTGAATGGGAACTTCAGCATGTGGCATCTCCAGTTTCTCTACT	420
Qy	1140	GGCACCAATACACACAGCGGTGAGACATTTGGCGTTGTGGTGACGCTTTCTTCCAAAACA	1199
Db	421	GGCACCAATACACACAGCGGTGAGACATTTGGCGTTGTGGTGACGCTTTCTTCCAAAACA	480
Qy	1200	CACCTCACCCCACTGAACGAGAGGGGACACTGACCTCACCTCTCTCTCGAGGACTGTT	1259
Db	481	CACCTCACCCCACTGAACGAGAGGGGACACTGACCTCACCTCTCTCTCGAGGACTGTT	540
Qy	1260	TTCACTTCTCAGACCGCGGCATGCCAGATGGCCATCGCACTCTGGAACAACATGCTGG	1319
Db	541	TTCACTTCTCAGACCGCGGCATGCCAGATGGCCATCGCACTCTGGAACAACATGCTGG	600
Qy	1320	AACGAGTGGGCGCAGACTTACCTCAACAACATTCACCACAGCCGAGGCCAACTCAAGT	1379
Db	601	AACGAGTGGGCGCAGACTTACCTCAACAACATTCACCACAGCCGAGGCCAACTCAAGT	660
Qy	1380	GCCTCTCTCTGAGAGCCCTTACCTCTACACCTCTCGGAAACAGCCGATGTCTCCAGACC	1439
Db	661	GCCTCTCTCTGAGAGCCCTTACCTCTACACCTCTCGGAAACAGCCGATGTCTCCAGACC	720
Qy	1440	AGGCTGAAGAACCCCGAGGTGCTTACTTGGGCTGTCCAGTGGCAGCGGAGTCCGGCC	1499
Db	721	AGGCTGAAGAACCCCGAGGTGCTTACTTACTTGGGCTGTCCAGTGGCAGCGGAGTCCGGCC	780
Qy	1500	TTGTGTGGGCATCATCGGACAGTGTCTGTGAGGTGCGAGAGAGGTGGCCGAGGGAAG	1559
Db	781	TTGTGTGGGCATCATCGGACAGTGTCTGTGAGGTGCGAGAGAGGTGGCCGAGGGAAG	840
Qy	1560	ATCTCTCAATGAGCTCGCACATGTGGCCCTCTAGGCCCGGGGTGGTCTCAACCCCTAA	1619
Db	841	ATCTCTCAATGAGCTCGCACATGTGGCCCTCTAGGCCCGGGGTGGTCTCAACCCCTAA	900
Qy	1620	ACTCCCTATAGCCACTCTCTTTCACCGCCCTCTGCCCGAGCCACTCCCGGCCACGAGACA	1679
Db	901	ACTCCCTATAGCCACTCTCTTTCACCGCCCTCTGCCCGAGCCACTCCCGGCCACGAGACA	960
Qy	1680	TGCTTCAATGCCCTGGTGCATAGGAAGCCAGGGGAACGTGCACAACTTCTTGGGGCTCGG	1739
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Qy	1740	GCCTTCTCCAGGCTATGCTCTCTGGATGATATTAATTAAGTCCAAAGCTATTTT	1799
Db	1021	GCCTTCTCCAGGCTATGCTCTCTGGATGATATTAATTAAGTCCAAAGCTATTTT	1080
Qy	1800	A 1800	

[illegible]

Db 721 ACAGCCGAGTCTCCAGACAGGAGTGAAGAAACCCCGAGGGTCTTACTGGGCTGTCC 780
 Qy 1479 CAGTGGCA--CGGGAGTTCGGCTTGTGGGATCATTCGGGACAGT-GGTCTGGAGGT 1535
 Db 781 CAAGGCAAGGGGGAATCCGCCCCCTGTGTGGGATCTTTTGGAAAGTGGGGCTGGAGGT 840
 Qy 1536 GCAGAGAGGTGG---CCGGAGGGAAGATCTTCAATGAGCTGGGCACTGTGGCCCTCT 1592
 Db 841 GCAGAAAGAGTGGCCCCCAAGGGAATCTTCAAGGAGCCCTCGGCCCTTGGGCCCCC 900
 Qy 1593 AGGCCCGGGGTGGTCTCTACCC 1616
 Db 901 CATTAACCCGACGAGGCTCTATCC 924

RESULT 5
 BX349938/c
 LOCUS
 DEFINITION BX349938 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 cDNA clone CS0DC023YA08 3-PRIME, mRNA sequence.
 ACCESSION BX349938
 VERSION BX349938.1 GI:30371420
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 903)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 1474.f,
 and it belongs to a clone representative of this cluster. For more
 information about this cluster and the virtual cDNA, see
 http://www.genoscope.cns.fr/cdna?s=CS0BA10052A12_CS00473_2&c=1474.f

FEATURES
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 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Query Match 41.4%; Score 760.6; DB 5; Length 903;
 Best Local Similarity 92.6%; Pred. No. 1.4e-174;
 Matches 833; Conservative 0; Mismatches 26; Indels 41; Gaps 2;
 Qy 648 TTCTGAAGAGTCAACCCCTTACCTCTTGGCTTCTTACCAGCACTGGGAGGGACAG 707
 Db 903 TTGAAAGATTCAACCCCTTACCTCTTGGCTTCTTANCAAGCANTGGGAGGGACAG 844
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 Qy 768 ACCTGGTAGCGGAATGAAGAAACAGCCCGGACATCAACCTGGAGAAAGACTGGAGCTGG 827

Db 783 CCCTGGTAGAGCGAATGAAGAAACAGCNCAGACATCAACTGGGAGAAAGACTGGAGCTGG 724
 Qy 828 TCACACTCTTTCATTTGGGGTCAACGACTTGTGTCTTACTTGTGAGATCC----- 876
 Db 723 TCACACTCTTTCATTTGGGGTCAACGACTTGTGTCTTATNCTGTGAGAAATCCGGTAGGCCCCC 664
 Qy 877 -----GGAGGCCCACTTTGGCCACGGAAATATGTTTCAG 907
 Db 663 GACCAACCCCATGGGACCTTGAGAAAGAGAGGCCCACTTTGGCCAGGAATATGTTTCAG 604
 Qy 908 CACATCCAAAGGCGCTGGACATCTCTCTGAGAGCTCCCAAGGGCTTTCGTCAACGTG 967
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 Qy 968 GTGAGGCTCATGAGCTGGCTAGCTGTACAGGGCCAAAGCGGGAATATGTCATGCTG 1027
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 Db 483 GCAGCTCAGAAACAACTGCATCTTGGCTCAGACACTTCGCAAGCTCCCTGGAGAAAGCAAGAA 424
 Qy 1088 CTGGAAGAAAGTGAACCTGGAACTCCAGCATGGCATCTCCAGTTTCTCTACTGCGACCAA 1147
 Db 423 CTGAAGAAAGTGAACCTGGAACTCCAGCATGGCATCTCCAGTTTCTCTACTGCGACCAA 364
 Qy 1148 TACACACAGCTGAGGACTTTGCGTTGTGTGAGCTTCTTCTTCCAAACACACTCACC 1207
 Db 363 TACACACAGCTGAGGACTTTGCGTTGTGTGAGCTTCTTCTTCCAAACACACTCACC 304
 Qy 1208 CCACTGAACGAGAGAGGGGACACTGACCTCACTTCTTCTCCGAGGACTGTTTTCACTTC 1267
 Db 303 CCACTGAACGAGAGAGGGGACACTGACCTCACTTCTTCTCCGAGGACTGTTTTCACTTC 244
 Qy 1268 TCAGACCGCGGCTGCGAGATGGCCATCGCACTCTGGAACACATGCTGGAAACCACTG 1327
 Db 243 TCAGACCGCGGCTGCGAGATGGCCATCGCACTCTGGAACACATGCTGGAAACCACTG 184
 Qy 1328 GGCCGGAAGACTACTCTCAACAACTTCAACCAAGCGAGCGCAAACTCAAGTGCCTCT 1387
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 Qy 1388 CTTGAGAGCCCTTACCTCTTACCCCTCGGAACAGCCGATGCTCCAGACCAAGCTGAA 1447
 Db 123 CTTGAGAGCCCTTACCTCTTACCCCTCGGAACAGCCGATGCTCCAGACCAAGCTGAA 64
 Qy 1448 GAAGCCCCCGAGGTGCTTACTGGGCTGTCCAGTGGAGGAGTGGGCTTGTGGTG 1507
 Db 63 GAAGCCCCCGAGGTGCTTACTGGGCTGTCCAG-GGCAGGGGAGTGGGCTTTGGGGGG 5

RESULT 6
 BX349937/c
 LOCUS
 DEFINITION BX349937 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 cDNA clone CS0DC023YA08 3-PRIME, mRNA sequence.
 ACCESSION BX349937
 VERSION BX349937.2 GI:46289055
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 925)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 5, 2003 this sequence version replaced gi:30371419.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1474.f, and it belongs to a clone representative of this cluster. For more information about this cluster and the virtual cDNA, see http://www.genoscope.cns.fr/cdna?s=CS0BA1005ZA12_CS00473_1&c=1474.f

FEATURES

source
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/clone lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized." Location/Qualifiers
39.78; Score 729.2; DB 5; Length 925;
Query Match 91.28; Pred. No. 6.5e-167;
Best Local Similarity 0; Mismatches 35; Indels 47; Gaps 5;
Matches 846; Conservative 0;
629 CACACACATGCCCAATTTCTGAAGATTTCAACCTTACCTCTGCTTCTCTAC 688
925 CTCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 870
689 AGCACTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 748
869 AGGCACTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 812
749 ATGCCAGCCCGCTGGGAGCTGGTGAAGATGAAGATGAAGATGAAGATGAAG 808
811 ATGCCAGCCCGCTGGGAGCTGGTGAAGATGAAGATGAAGATGAAGATGAAG 752
809 GAGAAGACTGAAGTGGTCACTCTTCAATGGGGTCAACGACTTGTGTCAATGCT 868
751 AAGAAGACTGAAGTGGTCACTCTTCAATGGGGTCAACGACTTGTGTCAATGCT 692
869 GAGAATCC-----GGAGGCCCACTT 888
691 GAGATCCGGTAGGCCCCCGACCAACCCATGGGAGCTGAGAGGAGGAGGAGGAG 632
889 GGCACGGAATATGTTTCAACATCAACAGGCTTGGACATCTCTCTGAGGAGCTCC 948
631 GGCACGGAATATGTTTCAACATCAACAGGCTTGGACATCTCTCTGAGGAGCTCC 572
949 AAGGGCTTTCCTCAACGCTGGTGAAGTCAATGAGCTGGTACCTGTACCGAGGCAAG 1008
571 AAGGGCTTTCCTCAACGCTGGTGAAGTCAATGAGCTGGTACCTGTACCGAGGCAAG 512
1009 CGGGAATGTCATGCTGCACTCAGAACACTGCTTGCCTCAGACACTCGCAAG 1068
511 CGGGAATGTCATGCTGCACTCAGAACACTGCTTGCCTCAGACACTCGCAAG 452
1069 CTCCTCGAGAGCAAGAACTGAAGAAAGTGAATGAACTCGACATGGCATCTCCAG 1128
451 CTCCTCGAGAGCAAGAACTGAAGAAAGTGAATGAACTCGACATGGCATCTCCAG 392
1129 TTTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1188
391 TTTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 332
1189 CTTCCAAACACACTCAACCCCACTGAACGAGAGAGGAGGAGGAGGAGGAGGAG 1248
331 CTTCCAAACACACTCAACCCCACTGAACGAGAGAGGAGGAGGAGGAGGAGGAG 272
1249 CGAGGAGCTGTTTCACTTCTCAGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1308

271 CGAGGAGCTGTTTCACTTCTCAGACCCGGGAGTCCGAGATGGCCATCGCACTCTGGAA 212
1309 CAACATGCTGGAACCAAGTGGGCGCCCAAGATTAACCTCAACAACTTCAACCCAGCCGAGC 1368
211 CAACATGCTGGAACCAAGTGGGCGCCCAAGATTAACCTCAACAACTTCAACCCAGCCGAGC 152
1369 CAACATGCTGGAACCAAGTGGGCGCCCAAGATTAACCTCAACAACTTCAACCCAGCCGAGC 1428
151 CAACATGCTGGAACCAAGTGGGCGCCCAAGATTAACCTCAACAACTTCAACCCAGCCGAGC 92
1429 GCTCCACAGACAGGCTGAAGAGCCCGGAGGCTGCTTACTGGGCTGCTCCAGTGGGAGC 1488
91 GCTCCACAGACAGGCTGAAGAGCCCGGAGGCTGCTTACTGGGCTGCTCCAG-GGCAGC 33
1489 GAGAGTCGCGCTTGTGGTGGGCAATCATC 1516
32 GGGAGTCGCGCTTGTGGTGGGCAATC 5

RESULT 7

BX369782
LOCUS
DEFINITION
BX369782 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
cDNA clone CS0DC023YA08 5-PRIME, mRNA sequence.
ACCESSION
BX369782
VERSION
BX369782.2 GI:46569360
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (bases 1 to 822)
Li W.B., Gruber C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT
On May 8, 2003 this sequence version replaced gi:30441506.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1474.f,
and it belongs to a clone representative of this cluster. For more
information about this cluster and the virtual cDNA, see
http://www.genoscope.cns.fr/cdna?s=CS0BAG008ZF03_CS00694_1&c=1474.f

FEATURES

source
1. .822
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC023YA08"
/tissue type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized." Location/Qualifiers
38.08; Score 697.6; DB 5; Length 822;
Query Match 93.38; Pred. No. 3.3e-159;
Best Local Similarity 0; Mismatches 14; Indels 41; Gaps 2;
Matches 764; Conservative 0;
541 GGGAGCTCGACCAACAACTCCAGTACCTTACCCATCTTGGAGGGGACTCTTTGGAG 600
4 GGGAGCTCGACCAACAACTCCAGTACCTTACCCATCTTGGAGGGGACTCTTTGGAG 63
601 CATTTGGAGGGGAGTGGAACTTGGAGACTCACACCACTGCCCAACATTTCTGAAGAAGTT 660

ORIGIN

Query Match 38.08; Score 697.6; DB 5; Length 822;
Best Local Similarity 93.38; Pred. No. 3.3e-159;
Matches 764; Conservative 0; Mismatches 14; Indels 41; Gaps 2;
541 GGGAGCTCGACCAACAACTCCAGTACCTTACCCATCTTGGAGGGGACTCTTTGGAG 600
4 GGGAGCTCGACCAACAACTCCAGTACCTTACCCATCTTGGAGGGGACTCTTTGGAG 63
601 CATTTGGAGGGGAGTGGAACTTGGAGACTCACACCACTGCCCAACATTTCTGAAGAAGTT 660

Mon Mar 28 09:43:25 2005

and 380-383
TAG_L1B=UI-CF-EC1
TAG_SEQ=AAGTGCTTAC"

932 CTCTCTGAGGAGCTCCCAA-GGGCTTTCTGCTCAACT-GGTGGAGTCAATGAGCT-GGCT 988
813 CTCTCTGAGGAGCTCCCAAGGGGCTTTCTCACTGGGTGGAGGCAATGAGCTGGCT 872
989 AGCTGTATACAGGCGCAAGCGGGAAA 1015
873 AGCTGTATACAGGCGCAAGCGGGAAA 899

RESULT 9
BU683311/c 716 bp mRNA linear EST 07-OCT-2002
LOCUS UI-CF-EC1-ace-k-16-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
DEFINITION UI-CF-EC1-ace-k-16-0-UI 3', mRNA sequence.

ACCESSION BU683311
VERSION BU683311.1 GI:23535131

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 716)
Bonaldo, M.F., Lennon, G. and Soares, M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene

JOURNAL Genome Res. 6 (9), 791-806 (1996)

PUBMED 97044477

COMMENT 8889548

Contact: McCray, PB

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.research.com) or from Open Biosystems

(www.openbiosystems.com).

The following repetitive elements were found in this cDNA

sequence: 1-24, >AT rich#Low_complexity

Seq primer: M13 FORWARD

POLYA-Yes

Location/Qualifiers

1. 716

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-CF-EC1-ace-k-16-0-UI"

/tissue_type="Lung"

/dev_stage="Adult and Fetal"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_lib="UI-CF-EC1"

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Best Local Similarity 90.1%; Pred No. 3.3e-142;
Matches 713; Conservative 0; Mismatches 3; Indels 75; Gaps 1;

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716 GGCAGCTCAGAAACAACCTGCTGCTCAGACATCGCAAAAGCTCCCTGGAGAGCAAGA 657

1087 ACTGAAGAAAGTGAACCTCCAGCATCGCAATCTCCAGTTTCTCTACTGSCACCA 1146

656 ACTGAAGAAAGTGAACCTCCAGCATCGCAATCTCCAGTTTCTCTACTGSCACCA 597

1147 ATACACACAGCGTGAGGACTTTGCGTTGTGTGAGCGCTTCTTCCAAAACACACTCAC 1206

596 ATACACACAGCGTGAGGACTTTGCGTTGTGTGAGCGCTTCTTCCAAAACACACTCAC 537

1207 CCCACTGAACGAGAGGGGACACTGACCTTCTTCTCCGAGGACTGTTTTCACCT 1266

536 CCCACTGAACGAGAGGGGACACTGACCTTCTTCTCCGAGGACTGTTTTCACCT 477

1267 CTCAGACCGCGGGCATGCCGAGATGGCCATCGCATCTCTGGAACAACACTGCTGGAACCACT 1326

476 CTCAGACCGCGGGCATGCCGAGATGGCCATCGCATCTCTGGAACAACACTGCTGGAACCACTG 428

1327 GGGCGGCAAGACTTACCTCCAACTTCCACCCACAGCGAGCAAACTCAAGTGCCTC 1386

427 -----

1387 TCCTGAGAGCCCTTACCTCTACACCTTCGGAACAGCGAGTTCCTCCAGACAGGCTGA 1446

427 -----GAGAGCCCTTACCTCTACACCTTCGGAACAGCGAGTTCCTCCAGACAGGCTGA 372

1447 AGAAGCCCCGAGGTGCTTACTGGGTGTCCTGAGTGCAGCGGAGTTCGGCTTGTGGT 1506

371 AGAAGCCCCGAGGTGCTTACTGGGTGTCCTGAGTGCAGCGGAGTTCGGCTTGTGGT 312

1507 GGGCATATCGGGACAGTGGTCTGAGGTGCAGAGAGGTGGCGGAGGAGAGTCTCC 1566

311 GGGCATATCGGGACAGTGGTCTGAGGTGCAGAGAGGTGGCGGAGGAGAGTCTCC 252

1567 AATGAGCTGCGCATGTGGCCCTCTAGCGCGGGGTGGGTCTCACCCTTAAACTCCCT 1626

251 AATGAGCTGCGCATGTGGCCCTCTAGCGCGGGGTGGGTCTCACCCTTAAACTCCCT 192

1627 ATAGCCACTCTCTTACCGCCCTCTGCGCCAGCCACTCCCGGCCACAGGACATGCTCA 1686

191 ATAGCCACTCTCTTACCGCCCTCTGCGCCAGCCACTCCCGGCCACAGGACATGCTCA 132

1687 ATGCTTGGTGGCCATAGAAAGCCAGGGGACATGACACTTCTTGGGCTTGGGCTTCTT 1746

131 ATGCTTGGTGGCCATAGAAAGCCAGGGGACATGACACTTCTTGGGCTTGGGCTTCTT 72

1747 CCAGGCTATGCTTCTGGAATGATACATTTAAATAAAGTCCAAAGCTTATTTAAAAAA 1806

71 CCAGGCTATGCTTCTGGAATGATACATTTAAATAAAGTCCAAAGCTTATTTAAAAAA 12

1807 AAAAAAAAAA 1817

11 AAAAAAAAAA 1

RESULT 10

BI488437

LOCUS 603020936F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5191712 5',

DEFINITION mRNA sequence.

ACCESSION BI488437

VERSION BI488437.1 GI:15327665

823 bp mRNA linear EST 28-AUG-2001


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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL1479 row: 9 column: 09
High quality sequence stop: 808.
Location/Qualifiers
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/mol_type="mRNA"
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/clone="IMAGE:5191712"
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Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."
FEATURES
source
CA447656/c
LOCUS CA447656/c
DEFINITION UI-H-E10-ayf-c-03-0-UI-81 NCI CGAP_E10 Homo sapiens cDNA clone
CA447656
VERSION CA447656
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-24, >AT rich#Low_complexity
Seq primer: M13 FORWARD
POLYAs-fes.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="UI-H-E10-ayf-c-03-0-UI"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP E10"
/note="Organ: Left Pelvis; Vector: p7T73-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP E10 is a cDNA library containing the following
tissue(s): Chondrosarcoma. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p7T73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is AACTTGCAC.
TAG_LTB=UI-H-E10
FEATURES
source
566 CTGGAGGGGACAGCAGGACTAAATGTGGCAGCGGAGGGCCAGAGCTAGGACATGCC 625
754 AGCCAGGCGCTGGGACCTGGTAGCGGAATGAAAGAAACAGCCCGACATCAACCTGGAGAA 813
626 AGCCAGGCGCTGGGACCTGGTAGCGGATGAAAGAAACAGCCCGACATCAACCTGGAGAA 685
814 AGACTGGAAGCTGGTTCACACTCTTC-ATTGGGGTCAACGACTTGTGTTCATTACTGTGAGA 872
686 AGACTGGAAGCTGGTTCACACTCTTC-CAATTGGGGTCAACGACTTGTGTTCATTACTGTGAGA 745
873 ATCCGAGGGCCACTTGGCCACGGAATATGTTACGACATCAACAGAGCCCTGGACATCC 932
746 ATCCGAGGGCCACTTGGCCACGGAATATGTTACGACATCAACAGAG-CTTGGACATGC 804
933 TCTCTGAGGAGCTCCCAAG 951
805 TCTCTGAGGAGCTCCCAAG 823
RESULT 11
CA447656/c
LOCUS CA447656/c
DEFINITION UI-H-E10-ayf-c-03-0-UI-81 NCI CGAP_E10 Homo sapiens cDNA clone
CA447656
VERSION CA447656
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-24, >AT rich#Low_complexity
Seq primer: M13 FORWARD
POLYAs-fes.
Location/Qualifiers
1..625
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-E10-ayf-c-03-0-UI"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP E10"
/note="Organ: Left Pelvis; Vector: p7T73-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP E10 is a cDNA library containing the following
tissue(s): Chondrosarcoma. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p7T73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is AACTTGCAC.
TAG_LTB=UI-H-E10
FEATURES
source
Query Match 34.2%; Score 627.8; DB 4; Length 823;
Best Local Similarity 97.2%; Pred. No. 3.8e-142;
Matches 660; Conservative 0; Mismatches 17; Indels 2; Gaps 2;
Qy 274 CTTTGAACCACTTGAAGCAAAACAGAGACCTGGACCTGAGCAGAGATGCCCATCAC 333
Db 146 CTTTGAACCACTTGAAGCAAAACAGAGACCTGGACCTGAGCAGAGATGCCCATCAC 205
Qy 334 CTGTCCCACTCAGATGAGCCCTTCTGAGAACCCCTCGAATAGTAACTACATGATCCC 393
Db 206 CTGTCCCACTCAGATGAGCCCTTCTGAGAACCCCTCGAATAGTAACTACATGATCCC 265
Qy 394 CATCAAGCCAGCATTTGAGAACTGGGGCAGTGTCTCTGTGTACAGAGTGAAGGCTTC 453
Db 266 CATCAAGCCAGCATTTGAGAACTGGGGCAGTGTCTCTGTGTACAGAGTGAAGGCTTC 325
Qy 454 CAATAGTGTTCACACCTCTGTCCACAGCTCCGACAGCAGACATCAAGTGTGGCGC 513
Db 326 CAATAGTGTTCACACCTCTGTCCACAGCTCCGACAGCAGACATCAAGTGTGGCGC 385
Qy 514 CTTGGGTGACTCTCTGACTACAGCAGTGGGAGCTCGACCAACAACTCCAGTACCTACC 573
Db 386 CTTGGGTGACTCTCTGACTACAGCAGTGGGAGCTCGACCAACAACTCCAGTACCTACC 445
Qy 574 CACATCTTGGAGGGGACTCTCTTGGAGCATTTGGAGGGATGGGAACCTTGGAGCTCACAC 633
Db 446 CACATCTTGGAGGGGACTCTCTTGGAGCATTTGGAGGGATGGGAACCTTGGAGCTCACAC 505
Qy 634 CACATGCCCCAACATTTCTGAAGAAGTTCAACCTTACCTCTTGGCTTCTTACCAAGCAC 693
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Qy 694 CTGGAGGGGACAGCAGGACTAAATGTGGCAGCGGAGGGGCCAGAGCTAGGACATGCC 753
```


Mon Mar 28 09:43:25 2005

University of Iowa
375 Newton Road, 4156 MEBRE, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seq primer: M13 Reverse.

TAG_SEQ=ACACTTCAC

ORIGIN

Query Match 34.0%; Score 624; DB 6; Length 625;
Best Local Similarity 99.8%; Pred. No. 3e-141;
Matches 624; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1193 CAAACACACTCACCCCACTGAACAGAGAGGGGACACTGACCTACCTCTTCTCCGAG 1252
Db |||||||
QY 625 CAAACACACTCACCCCACTGAACAGAGAGGGGACACTGACCTACCTCTTCTCCGAG 566
Db |||||||

QY 1253 GACTGTTTTCACCTCTCAGACCGGGGCGATGCCAGATGCCATCGCACTCTGGAACAAC 1312
Db |||||||

QY 565 GACTGTTTTCACCTCTCAGACCGGGGCGATGCCAGATGCCATCGCACTCTGGAACAAC 506
Db |||||||

QY 1313 ATGCTGGAAACAGTGGGCGCGAAGACTTACCTCAACAACTTACCCACAGCGCGCAAA 1372
Db |||||||

QY 505 ATGCTGGAAACAGTGGGCGCGAAGACTTACCTCAACAACTTACCCACAGCGCGCAAA 446
Db |||||||

QY 1373 CTCAGTCCCTCTCTCTGAGAGCCCTTACCTCTACACCTCGGGAACAGCCGATTTGCTC 1432
Db |||||||

QY 445 CTCAGTCCCTCTCTCTGAGAGCCCTTACCTCTACACCTCGGGAACAGCCGATTTGCTC 386
Db |||||||

QY 1433 CCAGACAGGCTGAAGAGCCCGAGGTGCTTACTTGGGCTGTCCAGTGGCAGCGGA 1492
Db |||||||

QY 385 CCAGACAGGCTGAAGAGCCCGAGGTGCTTACTTGGGCTGTCCAGTGGCAGCGGA 326
Db |||||||

QY 1493 CTCGCTTGTGGTGGGATCATCGGACAGTGTCTTGGAGTGTGAGAGGTGGCGCG 1552
Db |||||||

QY 325 CTCGCTTGTGGTGGGATCATCGGACAGTGTCTTGGAGTGTGAGAGGTGGCGCG 266
Db |||||||

QY 1553 AGGGAGATCTTCAATAGCTGGGCACTGTGGCCCTCTAGGCCCGGGGGTGGTCTC 1612
Db |||||||

QY 265 AGGGAGATCTTCAATAGCTGGGCACTGTGGCCCTCTAGGCCCGGGGGTGGTCTC 206
Db |||||||

QY 1613 ACCTAAATCTCCTATAGGACCTCTTCAACCGCCCTCTGCCAGCCACTTCCCGGCGAC 1672
Db |||||||

QY 205 ACCTAAATCTCCTATAGGACCTCTTCAACCGCCCTCTGCCAGCCACTTCCCGGCGAC 146
Db |||||||

QY 1673 CAGGACATGTTCAATGCTGTGGCAGTAGGAAGCCAGGGGACAGTCAACTTCTGG 1732
Db |||||||

QY 145 CAGGACATGTTCAATGCTGTGGCAGTAGGAAGCCAGGGGACAGTCAACTTCTGG 86
Db |||||||

QY 1733 GGCTGGGCTTCTCAGGCTTATGCTCTGGAATGGATACATTTAAATAAGTCCAAAG 1792
Db |||||||

QY 85 GGCTGGGCTTCTCAGGCTTATGCTCTGGAATGGATACATTTAAATAAGTCCAAAG 26
Db |||||||

QY 1793 CTATTTTAAAAAATAAAAAAAAAAAAA 1817
Db |||||||

QY 25 CTATTTTAAAAAATAAAAAAAAAAAAA 1

RESULT 12
BM714799 607 bp mRNA linear EST 28-FEB-2002
LOCUS UI-E-EJ0-ahs-f-21-0-UI.r1 UI-E-EJ0 Homo sapiens cDNA clone
DEFINITION UI-E-EJ0-ahs-f-21-0-UI 5', mRNA sequence.

ACCESSION BM714799

VERSION 1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 607)

Bonaldi, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

JOURNAL 97044477

MEDLINE 889548

COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics

ORIGIN

Query Match 33.1%; Score 607; DB 4; Length 607;
Best Local Similarity 100.0%; Pred. No. 4.3e-137;
Matches 607; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 746 GACATGCCAGCCAGGCGCTGGGACCTGTGAGCGAATGAAAAACAGCCCGACATCAAC 805
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QY 1 GACATGCCAGCCAGGCGCTGGGACCTGTGAGCGAATGAAAAACAGCCCGACATCAAC 60
Db |||||||

QY 806 CTGGAGAAAGACTGGAAAGCTGGTCACTCTTTCATTTGGGGTCAACGACTTGTGTATTAC 865
Db |||||||

QY 61 CTGGAGAAAGACTGGAAAGCTGGTCACTCTTTCATTTGGGGTCAACGACTTGTGTATTAC 120
Db |||||||

QY 866 TGTGAGAATCCGAGGCCCACTTGGCCAGGGAATGTTCACACATCAACAGAGCCCTG 925
Db |||||||

QY 121 TGTGAGAATCCGAGGCCCACTTGGCCAGGGAATGTTCACACATCAACAGAGCCCTG 180
Db |||||||

QY 926 GACATCTCTCTGAGGAGCTCCCAAGGCTTTTCGTCACGCTGGTGGAGTCTGAGCTG 985
Db |||||||

QY 181 GACATCTCTCTGAGGAGCTCCCAAGGCTTTTCGTCACGCTGGTGGAGTCTGAGCTG 240.
Db |||||||

QY 986 GCTAGCTGTACCAAGGCCCAAGCGGGGAATGTGCCATCTGCGAGCTCAGAACCACTGC 1045
Db |||||||

QY 241 GCTAGCTGTACCAAGGCCCAAGCGGGGAATGTGCCATCTGCGAGCTCAGAACCACTGC 300
Db |||||||

QY 1046 ACTTGCCTCAGACTCGAAAGCTCCCTCGAGAGCAAGAACTGAAGAAAGTGAAGCTGG 1105
Db |||||||

QY 301 ACTTGCCTCAGACTCGAAAGCTCCCTCGAGAGCAAGAACTGAAGAAAGTGAAGCTGG 360
Db |||||||

QY 1106 AACCTCCAGCATGCACTCTCCAGTTTCTCTACTGGCACCACATACACAGCGCTGAGGAC 1165
Db |||||||

Db		361 AACCTCAGACATGCGACTCTCAGATTTCTCTTA CTGGCACCAATA CACA CAGCGTGAGGAC	420
Qy		1166 TTTTCGGTGTGTGCAGCCCTTTCTTCCA AAAACA CACTCA CCCCACTGA ACAGAGAGAGGG	1225
Db		421 TTTTCGGTGTGTGCAGCCCTTTCTTCCA AAAACA CACTCA CCCCACTGA ACAGAGAGAGGG	480
Qy		1226 GACACTGACCTCACCTTCTTCTCGAGGACTGT TTTCAC TTCTCAGA CC CGGGGCATGCC	1285
Db		481 GACACTGACCTCACCTTCTTCTCGAGGACTGT TTTCAC TTCTCAGA CC CGGGGCATGCC	540
Qy		1286 GAGATGCCCATCGCACTCTGGA ACAACATGCTGGA ACGAGTGGGCCGCAAGACTTACCCTCC	1345
Db		541 GAGATGCCCATCGCACTCTGGA ACAACATGCTGGA ACGAGTGGGCCGCAAGACTTACCCTCC	600
Qy		1346 AACAACT 1352 	
Db		601 AACAACT 607 	

[illegible]

Fax: 314 200 1010
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -41m13 fwd. ET from Amersham
 High quality sequence stop: 477.

FEATURES
SOURCE

RESULT 14
AW467395/0
LOCUS
DEFINITION

AW467395	AW467395.1	GI:7037501
AW467395	AW467395.1	GI:7037501

KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

ORGANISM
HOMO SAPIENS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer

Tumor Gene Index

JOURNAL
Unpublished (1997)

CONTACT: Robert Strauberg, Ph.D.
Email: csapbs-r@mail.nih.gov
Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center

Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -400p from Gibco

Query Match

[illegible]

Db	507	ACATGCTCGAACCGAGTGGGCGCAAGACTACTCCAACTTCAACCCACAGCCGAGCCA	448
Qy	1371	AACTCAAGTGGCCCTCTCTGAGAGCCCTTACCTCTACACCCCTCGGAAACAGCCGATTGC	1430
Db	447	AACTCAAGTGGCCCTCTCTGAGAGCCCTTACCTCTACACCCCTCGGAAACAGCCGATTGC	388
Qy	1431	TCCAGACCGAGCTGAAGAACCCCGAGGTGCTCTACTGGGCTGTCCCACTGGGAGCGG	1490
Db	387	TCCAGACCGAGCTGAAGAACCCCGAGGTGCTCTACTGGGCTGTCCCACTGGGAGCGG	328
Qy	1491	GAGTCGGCTTGTGGTGGGCATCATCGGACAGTGGTCTGAGGTGACAGGAGAGGTGGCC	1550
Db	327	GAGTCGGCTTGTGGTGGGCATCATCGGACAGTGGTCTGAGGTGACAGGAGAGGTGGCC	268
Qy	1551	GGAGGGAAGATCTCCCAATGAGCCTGCGCACTGTGGCCCTCTAGGCCCGGGGTGGGTCC	1610
Db	267	GGAGGGAAGATCTCCCAATGAGCCTGCGCACTGTGGCCCTCTAGGCCCGGGGTGGGTCC	208
Qy	1611	TCACCTTAACTCCCTATAGCCACTCTCTTACCGCCCTCTGCCCCAGCCACTCCCGGCC	1670
Db	207	TCACCTTAACTCCCTATAGCCACTCTCTTACCGCCCTCTGCCCCAGCCACTCCCGGCC	148
Qy	1671	ACCAGGACATGCTTCAATGCTGGTGGCCATAGGAGCCCGAGGACAGTCACTTCTTT	1730
Db	147	ACCAGGACATGCTTCAATGCTGGTGGCCATAGGAGCCCGAGGACAGTCACTTCTTT	88
Qy	1731	GGGGCTGGGCTTCTTCCAGGCTATGCTCTGGAAATGGATACATTTAAATAAAGTCCAA	1790
Db	87	GGGGCTGGGCTTCTTCCAGGCTATGCTCTGGAAATGGATACATTTAAATAAAGTCCAA	28
Qy	1791	AGCTATTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1817
Db	27	AGCTATTTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	1

Search completed: March 27, 2005, 03:40:32
Job time : 5924.96 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 25, 2005, 14:18:06 ; Search time 176 Seconds
(without alignments)
1037.221 Million cell updates/sec

Title: US-09-778-961-2

Perfect score: 2518

Sequence: 1 MRELVGSRDYTOEDFSVL.....RCRRGRRPPMSLRITVAL 472

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2518	100.0	472	5	ABP53556 Human pho
2	2492	99.0	1458	5	ABB09555 Human lip
3	2492	99.0	1458	6	AAE34440 Human lip
4	2488	98.8	1458	5	ABB09556 Human lip
5	2469	98.1	1216	5	AAE22860 Human pho
6	2407	95.6	1423	5	ABU65083 Human NOV
7	2407	95.6	1423	8	ADH42431 Novel hum
8	2387	94.8	1423	8	ADN61817 Human nov
9	2336.5	92.8	1419	5	ABU65081 Human NOV
10	2336.5	92.8	1419	8	ADH42427 Novel hum
11	2336.5	92.8	1419	8	ADN61813 Human nov
12	2334.5	92.7	1433	8	ADO18815 Human lip
13	1715.5	68.1	1450	2	AAW30751 Rat phosp
14	1185	47.1	267	4	AAW25824 Human pro
15	1185	47.1	267	4	ABB11053 Human pho
16	884.5	35.1	937	8	ADH13664 Human ENZ
17	884.5	35.1	969	6	AAE34448 Human lip
18	884.5	35.1	1004	8	ADO18816 Human lip
19	599.5	23.8	382	8	ADN24372 Bacterial
20	551.5	21.9	414	8	ADN22922 Bacterial
21	527	20.9	101	5	ABB89352 Human pol
22	527	20.9	148	4	AAW95420 Human rep
23	527	20.9	148	4	ABB96111 Human tes
24	521	20.7	424	4	ABB71556 Drosophil
25	504	20.0	447	4	ABB65406 Drosophil

26	465.5	18.5	270	6	ADA54461 Human pro
27	456.5	18.1	310	5	ABU65082 Human NOV
28	456.5	18.1	310	8	ADH42429 Novel hum
29	455.5	18.1	310	8	ADN61815 Human nov
30	452.5	18.0	310	8	ADH42425 Novel hum
31	414	16.4	981	8	ADN22763 Bacterial
32	406.5	16.1	348	8	ADN23870 Bacterial
33	336.5	13.4	349	8	ADN23869 Bacterial
34	329	13.1	425	8	ADN22508 Bacterial
35	324.5	12.9	334	4	ABG02997 Novel hum
36	249	9.9	109	4	AAE10214 Human bon
37	233.5	9.3	132	4	ABB11237 Human pho
38	113	4.5	305	8	ADR41635 Lipid acy
39	113	4.5	305	8	ADR41585 Lipid acy
40	108	4.3	746	7	AAO30422 Human sec
41	108	4.3	759	7	AAO30421 Human sec
42	108	4.3	1083	8	ABM82537 Human dia
43	108	4.3	1084	8	ABM82536 Human dia
44	108	4.3	1099	8	ABM82535 Human dia
45	108	4.3	1112	8	ABM82534 Human dia

ALIGNMENTS

RESULT 1
ABP53556
ID ABP53556 standard; protein; 472 AA.
XX
AC ABP53556;
XX
DT 16-DEC-2002 (first entry)
XX
DB Human phospholipase protein SEQ ID NO:2.
XX
KW Human; phospholipase; enzyme; chromosome 2.
XX
OS Homo sapiens.
XX
PN WO200262977-A2.
XX
PD 15-AUG-2002.
XX
PF 28-JAN-2002; 2002WO-US002302.
XX
PR 08-FEB-2001; 2001US-00778961.
XX
PE (PEKE) PE CORP NY.
XX
PI Yan C, Ketchum KA, Di Francesco V, Beasley EM;
XX
WPI; 2002-682698/73.
XX
N-PSDB; ABQ82234.

New human phospholipase proteins, useful for the development of human therapeutics and diagnostic compositions, drug screening assays, tissue typing and pharmacogenomic analysis.

Claim 1; Fig 2A; 95pp; English.

The present sequence represents a human phospholipase protein (I) located on chromosome 2. (I) can be used for identifying agents that modulate its function or activity where the agent is useful for treating a disease or protein in biological fluids, and as markers for tissues where the condition mediated by a the human phospholipase protein. (I) peptides can be used in substantial and specific assays related to functional information of the peptide sequences, to raise antibodies or to elicit immune response, as reagents in assays that determine the levels of protein in biological fluids, and as markers for tissues where the corresponding protein is expressed. Nucleotide sequences encoding (I) can be used as probes, primers and chemical intermediates in biological assays, for constructing recombinant vectors, and expressing antigenic portions of the protein. (I) and nucleic acid molecules encoding it can be used in the identification of therapeutic proteins and may serve as

Mon Mar 28 09:43:26 2005

CC models or targets for the development of human therapeutic agents that
 CC modulate phospholipase activity in cells and tissues that express the
 CC phospholipase, such as in kidney, blood, lung, brain glioblastomas,
 CC prostate, colon or leukocytes
 XX
 SQ Sequence 472 AA;
 Query Match 100.0%; Score 2518; DB 5; Length 472;
 Best Local Similarity 100.0%; Pred. No. 6e-232;
 Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRELVGSGRYDQEDSVVLPQFQNIQVLALEPLGSKTETDLRAEMPITCPTQNEP 60
 DB 1 MRELVGSGRYDQEDSVVLPQFQNIQVLALEPLGSKTETDLRAEMPITCPTQNEP 60
 QY 61 FLTPRNSNTYPIKPAIENWGSDFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLT 120
 DB 61 FLTPRNSNTYPIKPAIENWGSDFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLT 120
 QY 121 AVGARPNSSDLPTSWRGLSISGSGNLETHHTLNLKKNPYPYLLGFSTSTWGTAGL 180
 DB 121 AVGARPNSSDLPTSWRGLSISGSGNLETHHTLNLKKNPYPYLLGFSTSTWGTAGL 180
 QY 181 NVAAEGARADMPAQAWDLVERMKNSPDINLEKDWKLVTFLIGVNDLCHYCENPEHLAT 240
 DB 181 NVAAEGARADMPAQAWDLVERMKNSPDINLEKDWKLVTFLIGVNDLCHYCENPEHLAT 240
 QY 241 EYVHQIQALDILSELPRAFVNVVMEASLYQGGGKCMALAAQNNCTCLRHSQSSL 300
 DB 241 EYVHQIQALDILSELPRAFVNVVMEASLYQGGGKCMALAAQNNCTCLRHSQSSL 300
 QY 301 EQKELKKNWNLQHGSISSFSYWHQYQREDFAVVVQPFQNTLPLNERGDTLTFPSED 360
 DB 301 EQKELKKNWNLQHGSISSFSYWHQYQREDFAVVVQPFQNTLPLNERGDTLTFPSED 360
 QY 361 CFHFSDRGHAEMAIALWNNMLEPVGRKTSNNFTHSRKAKLCPSPESPLYTLNLSLLP 420
 DB 361 CFHFSDRGHAEMAIALWNNMLEPVGRKTSNNFTHSRKAKLCPSPESPLYTLNLSLLP 420
 QY 421 DQAEAPVLYWAPVAAAGVLVGIIGTVVWRCRGRREDPPMSLRTVAL 472
 DB 421 DQAEAPVLYWAPVAAAGVLVGIIGTVVWRCRGRREDPPMSLRTVAL 472
 RESULT 2
 ABB09555
 ID ABB09555 standard; protein; 1458 AA.
 XX AC ABB09555;
 XX DT 21-OCT-2002 (first entry)
 XX DE Human lipase NHL (Ala 1318 variant).
 KW Human; lipase; chromosome 2; phospholipase B homologue; thyroid; brain;
 KW inflammatory disease; proliferative disease; infectious disease;
 KW clotting disorder; cancer; drug screening; mental disorder; NHL;
 KW diagnostic reagent; clinical trial monitoring; cosmetic; nutritional;
 KW mutation detection; gene expression analysis; transgenic animal;
 KW nontropic; cytostatic; antiinflammatory; single nucleotide polymorphism;
 KW SNP; gene therapy; enzyme.
 XX OS Homo sapiens.
 XX PH Key Location/Qualifiers
 FT Misc-difference 1318
 FT /note= "Val replaces Ala in a polymorphic variant
 FT (ABB09556)"
 XX WO200259328-A1.
 XX 01-AUG-2002.
 XX

PF 22-JAN-2002; 2002WO-US0001715.
 XX 24-JAN-2001; 2001US-0264049P.
 XX (LEXI-) LEXICON GENETICS INC.
 PA Yu X, Miranda M, Turner CA;
 XX WPI; 2002-599797/64.
 XX N-PSDB; ABQ7623.
 XX Polynucleotides encoding human lipases that are structurally related to
 XX animal lipases, particularly phospholipase B, useful for drug screening,
 XX diagnosis and in gene therapy of biological disorders.
 XX Claim 2; Page 37-41; 44pp; English.
 XX The invention relates to a novel human lipase (NHL; ABB09555, ABB09556)
 XX and to nucleic acids encoding it (ABQ7623, ABQ7624). The NHL has
 XX structural similarity with animal lipases, particularly phospholipase B.
 XX Polynucleotides encoding NHL were obtained using human genomic sequences
 XX in conjunction with human thyroid and brain cDNAs. The NHL gene is
 XX located on chromosome 2, and contains a C/T polymorphism at position 3953
 XX of the open reading frame (ORF), resulting in an Ala/Val substitution at
 XX position 1318 in the protein. NHL nucleotides and proteins are useful for
 XX treating disorders such as inflammatory or proliferative disease, as used
 XX in screening for compounds useful in the treatment of mental, biological
 XX or medical disorders, as diagnostic reagents, in clinical trial
 XX monitoring and in cosmetic and nutraceutical applications. NHL
 XX nucleotides can additionally be used in the detection of disease-
 XX associated mutations, in the analysis of gene expression, for the
 XX recombinant expression of NHL, to generate transgenic animals, in gene
 XX therapy, and as part of ribozyme and/or triple helix sequences useful in
 XX the modulation of NHL gene expression. The present sequence represents
 XX the Ala 1318 variant of NHL
 XX
 SQ Sequence 1458 AA;
 Query Match 99.0%; Score 2492; DB 5; Length 1458;
 Best Local Similarity 93.7%; Pred. No. 1.2e-228; Indels 32; Gaps 1;
 Matches 472; Conservative 0; Mismatches 0;
 QY 1 MRELVGSGRYDQEDSVVLPQFQNIQVLA----- 33
 DB 955 MRELVGSGRYDQEDSVVLPQFQNIQVLA----- 1014
 QY 34 -----LEPLGSKTETDLRAEMPITCPTQNEPFLTPRNSNTYPIKPAIENWGSDFLCT 88
 DB 1015 LWTNMLEPLGSKTETDLRAEMPITCPTQNEPFLTPRNSNTYPIKPAIENWGSDFLCT 1074
 QY 89 EWKASNSVPTSVHQLRPADIKVVAALGDSLTAVGARPNSSDLPTSWRGLSISGSGDN 148
 DB 1075 EWKASNSVPTSVHQLRPADIKVVAALGDSLTAVGARPNSSDLPTSWRGLSISGSGDN 1134
 QY 149 LETHHTLNLKKNPYPYLLGFSTSTWGTAGLVNVAEGARADMPAQAWDLVERMKNSPD 208
 DB 1135 LETHHTLNLKKNPYPYLLGFSTSTWGTAGLVNVAEGARADMPAQAWDLVERMKNSPD 1194
 QY 209 INLEKDWKLVTFLIGVNDLCHYCENPEHLATYVQHIQOALDILSELPRAFVNVVYM 268
 DB 1195 INLEKDWKLVTFLIGVNDLCHYCENPEHLATYVQHIQOALDILSELPRAFVNVVYM 1254
 QY 269 ELASLYQGGGKCMALAAQNNCTCLRHSQSSLKQELKKNWNLQHGSISSFSYWHQYTOR 328
 DB 1255 ELASLYQGGGKCMALAAQNNCTCLRHSQSSLKQELKKNWNLQHGSISSFSYWHQYTOR 1314
 QY 329 EDFAVVQPFQNTLPLNERGDTLTFPSEDCHFSRGRHAEMAIALWNNMLEPVGRKT 388
 DB 1315 EDFAVVQPFQNTLPLNERGDTLTFPSEDCHFSRGRHAEMAIALWNNMLEPVGRKT 1374
 QY 389 TSNNTFTHSRKAKLCPSPESPLYTLNLSRLLPQAEPEVLYWAPVAAAGVLVGIIG 448


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Db      1375 TSNPHTHRAKLCBPSPPSYLTURNSRLLPDQAEAPVLYWAPVAAGVLVVGIIIG 1434
Qy      449 TVWRCRGGRREDPPMSLRITVAL 472
      |||||
Db      1435 TVWRCRGGRREDPPMSLRITVAL 1458
      |||||

RESULT 3
ID      AAE34440 standard; protein; 1458 AA.
AC      AAE34440;
XX      14-MAY-2003 (first entry)
XX      Human lipid-associated molecule (LIPAM)-1 protein.
DE      Human; lipid-associated molecule; LIPAM; cardiovascular disorder; stroke;
KW      arteriovenous fistula; atherosclerosis; hypertension; Raynaud's disease;
KW      aneurysm; congestive heart failure; thrombophlebitis; angina pectoris;
KW      ischaemic heart disease; rheumatic heart disease; peptic oesophagitis;
KW      gastrointestinal disorder; lipid metabolism disorder; Crohn's disease;
KW      nausea; peptic ulcer; fatty liver; Fabry's disease; Gaucher's disease;
KW      diabetes mellitus; hyperlipidaemia; hypercholesterolaemia; epilepsy;
KW      autoimmune disorder; inflammatory disorder; neurological disorder; kuru;
KW      acquired immunodeficiency syndrome; anaemia; Alzheimer's disease; asthma;
KW      dementia; prion disease; Creutzfeldt-Jakob disease; leukaemia; cancer;
KW      adenocarcinoma; lymphoma; melanoma; myeloma; sarcoma; gene therapy;
KW      protein replacement therapy.
XX      Homo sapiens.
OS      Homo sapiens.
FH      Key
FT      Peptide
FT      1. .27
FT      /label= Signal-peptide
FT      1. .23
FT      /label= Signal-peptide
FT      1. .22
FT      /label= Signal-peptide
FT      1. .21
FT      /label= Signal-peptide
FT      1. .19
FT      /label= Signal-peptide
FT      20. .1458
FT      /note= "Human mature LIPAM-1 protein"
FT      22. .1458
FT      /note= "Human mature LIPAM-1 protein"
FT      23. .1458
FT      /note= "Human mature LIPAM-1 protein"
FT      24. .1458
FT      /note= "Human mature LIPAM-1 protein"
FT      28. .1458
FT      /note= "Human mature LIPAM-1 protein"
FT      393. .521
FT      /note= "Lipase/acylhydrolase with GDSL-like motif"
FT      394. .404
FT      /note= "Lipolytic enzyme G-D-S-L family serine active-
FT      site"
FT      740. .868
FT      /note= "Lipase/acylhydrolase with GDSL-like motif"
FT      741. .751
FT      /note= "Lipolytic enzyme G-D-S-L family serine active-
FT      site"
FT      1096. 1219
FT      /note= "Lipase/acylhydrolase with GDSL-like motif"
FT      1415. .1442
FT      /note= "Transmembrane domain"
XX      WO200294988-A2.
XX      28-NOV-2002.
XX      17-MAY-2002; 2002WO-US015688.

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XX      18-MAY-2001; 2001US-0292242P.
PR      25-MAY-2001; 2001US-0293726P.
PR      01-JUN-2001; 2001US-0295346P.
PR      06-JUL-2001; 2001US-0303404P.
PR      24-AUG-2001; 2001US-0314754P.
PR      22-JAN-2002; 2002US-0351262P.
PR      29-MAR-2002; 2002US-0368799P.
XX      (INCY-) INCYTE GENOMICS INC.
XX      Tang YT, Yue H, Azimzai Y, Baughn MR, Burford N, Reddy R;
PI      Walia NK, Das D, Nguyen DB, Arvizu CS, Lu Y, Gandhi AR;
PI      Griffin JA, Elliott VS, Ramkumar J, Lal PG, Lu DAM, Lee SY;
XX      Yue H, Yang J, Tribouley CM, Kabie AE, Swarnakar A;
XX      WPI; 2003-120797/11.
DR      N-PSDB; AAD52626.
XX      New human lipid-associated molecule (LIPAM) proteins and polynucleotides,
XX      useful for diagnosing, treating or preventing cardiovascular disorders
XX      (e.g. aneurysms), neurological disorders (e.g. Parkinson's disease) or
XX      cancers.
XX      Claim 56; Page 137-141; 171pp; English.
XX      The present invention relates to novel human lipid-associated molecules
XX      (LIPAM) and polynucleotides encoding such proteins. Sequences of the
XX      invention are useful for treating diseases or conditions associated with
XX      decreased expression of functional LIPAM. The antagonist is useful for
XX      treating a disease or condition associated with the overexpression of
XX      functional LIPAM. They are useful for diagnosing, treating or preventing
XX      cardiovascular disorders (e.g. arteriovenous fistula, atherosclerosis,
XX      hypertension, Raynaud's disease, aneurysms, varicose veins, congestive
XX      heart failure, thrombophlebitis, angina pectoris, ischaemic heart disease
XX      or rheumatic heart disease), gastrointestinal disorders (e.g. peptic
XX      oesophagitis, nausea, peptic ulcer or Crohn's disease), lipid metabolism
XX      disorders (e.g. fatty liver, Fabry's disease, Gaucher's disease, diabetes
XX      mellitus, hyperlipidaemia, hypercholesterolaemia), autoimmune disorders
XX      or inflammatory disorders (e.g. acquired immunodeficiency syndrome,
XX      anaemia, asthma or Crohn's disease), neurological disorders (e.g. stroke,
XX      epilepsy, dementia, Alzheimer's disease, or prion diseases such as kuru
XX      or Creutzfeldt-Jakob disease) or cancers (e.g. adenocarcinoma, leukaemia,
XX      lymphoma, melanoma, myeloma or sarcoma). They are also used in gene
XX      therapy and protein replacement therapy. The present sequence is human
XX      LIPAM-1 protein
XX      SQ      Sequence 1458 AA;
XX      Query Match          99.0%; Score 2492; DB 6; Length 1458;
XX      Best Local Similarity 93.7%; Pred. No. 1.2e-228;
XX      Matches 472; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
Qy      1 MRELVGSGRYDTQEDFSVVLQPPFQNIQLPVL----- 33
Db      955 MRELVGSGRYDTQEDFSVVLQPPFQNIQLPVLADGLDPTSPFAPDCIHPNOKFHSQLARA 1014
Qy      34 -----LSPLGSKTETLDRAEMPTTCPTONEPFLTRPNSNYTPIKPAIENWGSDFLCT 88
Db      1015 LWTNMLSPGSKTETLDRAEMPTTCPTONEPFLTRPNSNYTPIKPAIENWGSDFLCT 1074
Qy      89 EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSDLPTSWRGLSWSIGDGN 148
Db      1075 EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSDLPTSWRGLSWSIGDGN 1134
Qy      149 LETHHTLTPNLIKKNPNVLLGFSTSTWEGTAGLVNAAGARADMPAQAWDLVERMKNSPD 208
Db      1135 LETHHTLTPNLIKKNPNVLLGFSTSTWEGTAGLVNAAGARADMPAQAWDLVERMKNSPD 1194
Qy      209 INLEKDWKLVTLFTGVNDLCHYCNPEAHLATEVVOHIQQALDILSELPRAFVNVVEVM 268
Db      1195 INLEKDWKLVTLFTGVNDLCHYCNPEAHLATEVVOHIQQALDILSELPRAFVNVVEVM 1254

```

in screening for compounds useful in the treatment of mental, biological or medical disorders, as diagnostic reagents, in clinical trial monitoring and in cosmetic and nutraceutical applications. NHL nucleotides can additionally be used in the detection of disease-associated mutations, in the analysis of gene expression, for the recombinant expression of NHL, to generate transgenic animals, in gene therapy, and as part of ribozyme and/or triple helix sequences useful in the modulation of NHL gene expression. The present sequence represents the Val 1318 variant of NHL. Note: The present sequence is not shown in the specification, but was derived from the information given on page 18 and the Ala 1318 NHL variant (ABB09555) given in the sequence listing

Query Match	98.8%;	Score	2488;	DB	5;	Length	1458;
Best Local Similarity	93.5%;	Pred. No.	2.8e-228;				
Matches	471;	Conservative	0;	Mismatches	1;	Indels	32;
						Gaps	1;
Qy	1	MRELVSGRYDQEDSVVLQPPFQNIQLPVLA-----	33				
Db	955	MRELVSGRYDQEDSVVLQPPFQNIQLPVLADGLPDTSPFAPDCIHPNQKFHSQARA	1014				
Qy	34	-----LEPLGSKTETLDLRAEMPICTPTQNEPFLRTPRNSNYTPIKPAIENWGSDFLCT	88				
Db	1015	LWTNMLEPLGSKTETLDLRAEMPICTPTQNEPFLRTPRNSNYTPIKPAIENWGSDFLCT	1074				
Qy	89	EWKASNSVPPTS VHQLRPADIKVVAALGDSLTTVAGARPNNSSDLPTPSWGLSWISIGDGN	148				
Db	1075	EWKASNSVPPTS VHQLRPADIKVVAALGDSLTTVAGARPNNSSDLPTPSWGLSWISIGDGN	1134				
Qy	149	LETHTTTLPNILKKFNPVLLGFSTWEGTAGLVAAEGARADMPAQAWDLVERMKNSPD	208				
Db	1135	LETHTTTLPNILKKFNPVLLGFSTWEGTAGLVAAEGARADMPAQAWDLVERMKNSPD	1194				
Qy	209	INLEKWKLVTLFTIGVNDLCHYCENPAHLATEYVQHIQQALDILSEELPRAFWNVVEVM	268				
Db	1195	INLEKWKLVTLFTIGVNDLCHYCENPAHLATEYVQHIQQALDILSEELPRAFWNVVEVM	1254				
Qy	269	ELASLYQOGGKCAMLAAQNNCTCLRHSQSLEKEQLKKNWNLOHGISFSFYHWQYTOR	328				
Db	1255	ELASLYQOGGKCAMLAAQNNCTCLRHSQSLEKEQLKKNWNLOHGISFSFYHWQYTOR	1314				
Qy	329	EDFAVVPVPPFQNTLTPLNERGDDTLTFSSDCDFHSDRGHAEMAIALWNNMLEPVGKRT	388				
Db	1315	EDFVVPVVPFQNTLTPLNERGDDTLTFSSDCDFHSDRGHAEMAIALWNNMLEPVGKRT	1374				
Qy	389	TSNNFTHSRAKIKCPSPESPPLYTLRNSRLLPDQAEAEPEVLYWAVPVAGVGLVWGIIIG	448				
Db	1375	TSNNFTHSRAKIKCPSPESPPLYTLRNSRLLPDQAEAEPEVLYWAVPVAGVGLVWGIIIG	1434				
Qy	449	TVVWRCRGRGREDPPNGLRTVAL	472				
Db	1425	TVVWRCRGRGREDPPNGLRTVAL	1458				

RESULT 5	
AAE22860	
ID	AAE22860 standard; protein; 1216 AA.
XX	
XX	AAE22860;
XX	
DT	27-AUG-2002 (first entry)
XX	
D6	Human phospholipase-like enzyme.
XX	
KW	Human, phospholipase-like enzyme; cancer; inflammation; Pick's disease;
KW	cardiovascular disorder; central nervous system disorder; brain injury;
KW	chronic obstructive pulmonary disease; cerebrovascular disease; dementia;
KW	Alzheimer's disease; Parkinson's disease; corticobasal degeneration;
KW	motor neuron disease; Huntington's disease; Creutzfeldt Jacob dementia;
KW	schizophrenia; Korsakoff's psychosis; pain; epilepsy; multiple sclerosis;
KW	schiatrica; stroke; age associated memory impairment; allergy; asthma;
KW	allergic rhinitis; hay fever; atopic dermatitis; cardiovascular disease;

QY	269	ELASLYQGQGGKCAWLAQNNCTCLRHSSQSLEKQELKKVNNWLOHGISSFSYWHQYTOR	328
Db	1255	ELASLYQGQGGKCAWLAQNNCTCLRHSSQSLEKQELKKVNNWLOHGISSFSYWHQYTOR	1314
QY	329	EDFAVVVQPFQNTLTPLNERGDTLTFSSDCPHFSDRGHAEMALWNNMLEPVGRKT	388
Db	1315	EDFAVVVQPFQNTLTPLNERGDTLTFSSDCPHFSDRGHAEMALWNNMLEPVGRKT	1374
QY	389	TSNNFTHSRALKCPSPSPYLITLRSRLPDQAEAPVLYWAVPAAGVGLVWGIIIG	448
Db	1375	TSNNFTHSRALKCPSPSPYLITLRSRLPDQAEAPVLYWAVPAAGVGLVWGIIIG	1434
QY	449	TVVWRCRRGGRREDPPMSLRITVAL	472
Db	1435	TVVWRCRRGGRREDPPMSLRITVAL	1458
RESULT 4			
AB	BB09556	standard; protein; 1458 AA.	
XX	AC	ABB09556;	
XX	DT	21-OCT-2002 (first entry)	
XX	DE	Human lipase NHL (Val 1318 variant).	
XX	KW	Human; lipase; chromosome 2; phospholipase B homologue; thyroid; brain;	
KW	KW	inflammatory disease; proliferative disease; infectious disease;	
KW	KW	clotting disorder; cancer; drug screening; mental disorder; NHL;	
KW	KW	diagnostic reagent; clinical trial monitoring; cosmetic; nutraceutical;	
KW	KW	mutation detection; gene expression analysis; transgenic animal;	
KW	KW	neutropic; cytostatic; antiinflammatory; single nucleotide polymorphism;	
KW	KW	SNP; gene therapy; enzyme.	
XX	OS	Homo sapiens.	
XX	XX	Key Location/Qualifiers	
XX	FT	Misc-difference 1318	
FT	FT	/note= "Ala replaces Val in a polymorphic variant	
FT	FT	(ABB09555)"	
XX	FN	WO200259328-A1.	
XX	PD	01-AUG-2002.	
XX	PF	22-JAN-2002; 2002WO-US001715.	
XX	PR	24-JAN-2001; 2001US-0264049P.	
XX	PA	(LEXI-) LEXICON GENETICS INC.	
XX	PI	Yu X, Miranda M, Turner CA;	
XX	DR	WPI; 2002-599797/64.	
DR	DR	N-PSDB; ABQ77624.	
XX	XX	Polynucleotides encoding human lipases that are structurally related to	
PT	PT	animal lipases, particularly phospholipase B, useful for drug screening,	
PT	PT	diagnosis and in gene therapy of biological disorders.	
XX	PS	Disclosure; Page; 44pp; English.	
XX	CC	The invention relates to a novel human lipase (NHL; ABB09555, ABB09556)	
CC	CC	and to nucleic acids encoding it (ABQ77623, ABQ77624). The NHL has	
CC	CC	structural similarity with animal lipases, particularly phospholipase B.	
CC	CC	Polynucleotides encoding NHL were obtained using human genomic sequences	
CC	CC	in conjunction with human thyroid and brain cDNAs. The NHL gene is	
CC	CC	located on chromosome 2, and contains a C/T polymorphism at position 3953	
CC	CC	of the open reading frame (ORF), resulting in an Ala/Val substitution at	
CC	CC	position 1318 in the protein. NHL nucleotides and proteins are useful for	
CC	CC	treating disorders such as inflammatory or proliferative disease,	
CC	CC	infectious disease, clotting disorders, and cancer. They can also be used	

KW anaphylaxis; inflammation; acute respiratory distress syndrome; diabetes;
KW chronic obstructive pulmonary disease; emphysema; obesity; anorexia;
KW overweight; cachexia; bulimia; hypertension; coronary artery disease;
KW type-II diabetes; hyperlipidaemia; gall bladder disease; osteoarthritis;
KW gout; sleep apnoea; respiratory problem; polycystic ovarian syndrome;
KW thrombolytic disease; reduced fertility; pregnancy; stress incontinence;
KW hirsutism; menstrual irregularity; depression; enzyme.
XX
OS Homo sapiens.
XX WO200231161-A2.
XX PD 18-APR-2002.
XX PF 09-OCT-2001; 2001WO-EP011641.
XX PR 10-OCT-2000; 2000US-0238445P.
XX PR 26-DEC-2000; 2000US-0257293P.
XX PA (FARB) BAYER AG.
XX PI Zhu Z;
XX DR WPI; 2002-426287/45.
XX PT N-PSDB; AAD37410.
XX PS New human phospholipase-like enzyme polypeptide useful for screening
agents, and in the treatment of cancer, inflammation, diabetes, obesity,
a central nervous system disorder, or a cardiovascular disorder.
XX Claim 25; Fig 2; 144pp; English.

The present invention relates to novel human phospholipase-like enzymes
and polynucleotides encoding such proteins. Sequences of the invention
are useful for producing a medicament for modulating the activity of
phospholipase in a disease such as cancer, inflammation, cardiovascular
disorders, chronic obstructive pulmonary diseases, central nervous system
(CNS) disorders such as brain injuries, cerebrovascular disease, dementia
(Alzheimer's disease), Parkinson's disease, corticobasal degeneration,
motor neuron disease, Pick's disease, Huntington's disease, Creutzfeldt
Jacob dementia, schizophrenia with dementia, Korsakoff's psychosis, pain
associated with CNS (e.g. epilepsy, failed back surgery syndrome,
sciatica), multiple sclerosis, stroke, age associated memory impairment,
allergic disease including asthma, allergic rhinitis (hay fever), atopic
dermatitis, anaphylaxis and inflammation, cardiovascular disease, chronic
obstructive pulmonary disease, acute respiratory distress syndrome, gout,
diabetes, emphysema or obesity. They are also used for treating anorexia,
overweight, cachexia, bulimia, hypertension, type-II diabetes, coronary
artery disease, hyperlipidaemia, gall bladder disease, osteoarthritis,
sleep apnoea and respiratory problems, cancer (e.g. breast, prostate,
colon cancer), thrombolytic disease, reduced fertility, polycystic
ovarian syndrome, complications of pregnancy, menstrual irregularity,
hirsutism, stress incontinence and depression. The present sequence is
a human phospholipase like enzyme

SQ Sequence 1216 AA;

Query Match 98.1%; Score 2469; DB 5; Length 1216;
Best Local Similarity 93.0%; Pred. No. 1.4e-226;
Matches 466; Conservative 2; Mismatches 1; Indels 32; Gaps 1;

Qy 1 MRELVGSGRYDQEDFSVVLQFFQNTQLPVLVLA----- 33
Db 716 MRELVGSGRYDQEDFSVVLQFFQNTQLPVLVLA----- 33
Qy 34 -----LPLSGKTETDLRAEMPTCTQNEPFLTPRNSNYTPIKPAIENWGSDFLCT 88
Db 776 LWTNMLEPLSGKTETDLRAEMPTCTQNEPFLTPRNSNYTPIKPAIENWGSDFLCT 835
Qy 89 EWKASNSVPTSVHOLRPADIKVVAALGDSLTTAVGAPNNSSDLPTSWRGLSWISIGDGN 148-
Db 836 EWKASNSVPTSVHOLRPADIKVVAALGDSLTVSMGAPNNSSDLPTSWRGLSWISIGDGN 895

Qy 149 LETHTTLPNLKKNFNYLLGFSTWEGTAGLNVAAGARADMPAQAWDLVERMKNSPD 208
Db 896 LETHTTLPNLKKNFNYLLGFSTWEGTAGLNVAAGARADMPAQAWDLVERMKNSPD 955
Qy 209 INLEKDKWLTFLTGVDNLCHYCENPEAHILATEVVOHIQQALDILSEELPFAFVNVVVM 268
Db 956 INLEKDKWLTFLTGVDNLCHYCENPEAHILATEVVOHIQQALDILSEELPFAFVNVVVM 1015
Qy 269 ELASLYOGQGGKCAMLAAQNNCTCLRHQSQSLEKQELKKNVNNLQHGIGSSFSYWHQYTOR 328
Db 1016 ELASLYOGQGGKCAMLAAQNNCTCLRHQSQSLEKQELKKNVNNLQHGIGSSFSYWHQYTOR 1075
Qy 329 EDFAVVVOVPPFQNTLTPLNERGDTDLTFFSDCFHSDRGHAEMAIALWNNMLPVGKRT 388
Db 1076 EDFAVVVOVPPFQNTLTPLNERGDTDLTFFSDCFHSDRGHAEMAIALWNNMLPVGKRT 1135
Qy 389 TSNFTHSRAKLKCPSPESPVLYTLRNSRLLPDQAEAPVLYYAVPVAAGVGLVVGIIIG 448
Db 1136 TSNFTHSRAKLKCPSPESPVLYTLRNSRLLPDQAEAPVLYYAVPVAAGVGLVVGIIIG 1195
Qy 449 TVWRCRRGGRREDPPMSLRT 469
Db 1196 TVWRCRRGGRREDPPMSLRT 1216
RESULT 6
ABU65083
ID ABU65083 standard; protein; 1423 AA.
XX AC ABU65083;
XX DT 20-MAY-2003 (first entry)
XX DB Human NOV24c protein.
XX KW NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;
KW hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;
KW human.
XX OS Homo sapiens.
XX PN WO200272757-A2.
XX PD 19-SEP-2002.
XX PF 08-MAR-2002; 2002WO-US006908.
XX PR 08-MAR-2001; 2001US-0274101P.
PR 08-MAR-2001; 2001US-0274194P.
PR 08-MAR-2001; 2001US-0274281P.
PR 08-MAR-2001; 2001US-0274322P.
PR 09-MAR-2001; 2001US-0274849P.
PR 12-MAR-2001; 2001US-0275235P.
PR 13-MAR-2001; 2001US-0275578P.
PR 13-MAR-2001; 2001US-0275579P.
PR 14-MAR-2001; 2001US-0275601P.
PR 16-MAR-2001; 2001US-0276000P.
PR 16-MAR-2001; 2001US-0276776P.
PR 19-MAR-2001; 2001US-0276994P.
PR 20-MAR-2001; 2001US-0277239P.
PR 20-MAR-2001; 2001US-0277321P.
PR 20-MAR-2001; 2001US-0277327P.
PR 21-MAR-2001; 2001US-0277791P.
PR 22-MAR-2001; 2001US-0277833P.
PR 23-MAR-2001; 2001US-0278152P.
PR 26-MAR-2001; 2001US-0278894P.
PR 27-MAR-2001; 2001US-0278999P.
PR 27-MAR-2001; 2001US-0279036P.
PR 28-MAR-2001; 2001US-0279344P.
PR 30-MAR-2001; 2001US-0279338P.
PR 30-MAR-2001; 2001US-0279995P.
PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.

PR	02-APR-2001;	2001US-0280822P.	QY	1	MRELVSGRYDQEDFSVVLQPFQFQNIQLPVL	32
PR	04-APR-2001;	2001US-0280900P.	Db	924	MRELVSGRYDQEDFSVVLQPFQFQNIQLPVLQDGLPDTSPFADCIHPNQKHSQALARA	983
PR	04-APR-2001;	2001US-0281194P.	QY	33	----ALEPLGSKTETLDLRAEMPIITCPTQNEPFLRTPNNSYTYPIKPAIENMGSDFLCT	88
PR	13-APR-2001;	2001US-0283675P.	Db	984	LWTNMLEPLGSKTETLDLRAEMPIITCPTQNEPFLRTPNNSYTYPIKPAIENMGSDFLCT	1043
PR	03-MAY-2001;	2001US-0288066P.	QY	89	EWKASNSVPTSVHOLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWISGSDGN	148
PR	03-MAY-2001;	2001US-0288342P.	Db	1044	EWKASNSVPTSVHOLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWISGSDGN	1103
PR	15-MAY-2001;	2001US-0288528P.	QY	149	LETHHTLPLNLIKFNFPYLLGFSTSTWEGTAGLNVAAGARADMPAQAWDLVERMKNSP	207
PR	16-MAY-2001;	2001US-0291240P.	Db	1104	LETHHTLPLNLIKFNFPYLLGFSTSTWEGTAGLNVAAGARADMPAQAWDLVERMKNSPQ	1163
PR	30-MAY-2001;	2001US-0294485P.	QY	208	DINLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQALDILSBELEPRAFYVVEV	267
PR	31-MAY-2001;	2001US-0294899P.	Db	1164	DINLEKDWKLVTLFIGVNDLCHYCENP-----VGEYVQHIQQALDILSBELEPRAFYVVEV	1219
PR	18-JUN-2001;	2001US-0299027P.	QY	268	MELASLYQGGGKCMALAAQNCTCLRHQSQSLSEKOLKKVNNVNHQHGSSFSYHMYTO	327
PR	19-JUN-2001;	2001US-0299310P.	Db	1220	MELASLYQGGGKCMALAAQNCTCLRHQSQSLSEKOLKKVNNVNHQHGSSFSYHMYTO	1279
PR	31-JUL-2001;	2001US-0309198P.	QY	328	REDFAVVVQPFQNTLPLNERGDTLTFSEDCFFHSDRGHAEMAIALWNNMLEPVGK	387
PR	16-AUG-2001;	2001US-0312903P.	Db	1280	REDFAVVVQPFQNTLPLNERGDTLTFSEDCFFHSDRGHAEMAIALWNNMLEPVGK	1338
PR	10-SEP-2001;	2001US-0318462P.	QY	388	TTSNNFTHSRALKKCPSPESPILYTLNRSLLPDQAEAPVLYWAVPVAAGVGLVVGII	447
PR	27-SEP-2001;	2001US-0325430P.	Db	1339	TTSNNFTHSRALKKCPSPESPILYTLNRSLLPDQAEAPVLYWAVPVAAGVGLVVGII	1398
PR	14-NOV-2001;	2001US-0332272P.	QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472
PR	14-NOV-2001;	2001US-0333184P.	Db	1399	GTVVWRCRRGRRDPPMSLRTVAL	1423
PR	21-NOV-2001;	2001US-0332094P.	QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472
PR	03-DEC-2001;	2001US-0337426P.	Db	1399	GTVVWRCRRGRRDPPMSLRTVAL	1423
PR	03-DEC-2001;	2001US-0338092P.	QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472
PR	04-DEC-2001;	2001US-0337185P.	Db	1399	GTVVWRCRRGRRDPPMSLRTVAL	1423
PR	03-JAN-2002;	2002US-0345705P.	QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472
PR	07-MAR-2002;	2002US-00092900.	Db	1399	GTVVWRCRRGRRDPPMSLRTVAL	1423
PA	(CURA-) CURAGEN CORP.		QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472
PI	Padigar M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L;		Db	1399	GTVVWRCRRGRRDPPMSLRTVAL	1423
PI	Zernhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;		QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472
PI	Patturajan M, Gangolli E, Vernet CAM, Guo X, Tchernev V;		Db	1399	GTVVWRCRRGRRDPPMSLRTVAL	1423
PI	Fernandes ER, Casman SJ, Malyankar UM, Garlach V, Liu Y, Anderson D;		QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472
PI	Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobrook JP;		Db	1399	GTVVWRCRRGRRDPPMSLRTVAL	1423
PI	Lepley DM, Rieger DK;		QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472
DR	WPI; 2002-723332/78.		Db	1399	GTVVWRCRRGRRDPPMSLRTVAL	1423
DR	N-PSDB; ABX97050.		QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472
XX	NOVX polypeptides and polynucleotides, useful for preventing or treating		Db	1399	GTVVWRCRRGRRDPPMSLRTVAL	1423
XX	a disorder associated with aberrant NOVX expression or activity e.g.,		QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472
XX	cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial		Db	1399	GTVVWRCRRGRRDPPMSLRTVAL	1423
XX	asthma.		QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472
XX	Claim 1; Page 170; 1103pp; English.		Db	1399	GTVVWRCRRGRRDPPMSLRTVAL	1423
XX	This invention describes novel human NOVX polypeptides which have		QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472
XX	cytostatic, cardiac, antiarteriosclerotic, antiasthmatic and hypotensive		Db	1399	GTVVWRCRRGRRDPPMSLRTVAL	1423
XX	activity. Pharmaceutical compositions comprising the NOVX proteins or		QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472
XX	nucleic acid molecules or NOVX antibodies are useful for preventing or		Db	1399	GTVVWRCRRGRRDPPMSLRTVAL	1423
XX	treating a disorder associated with aberrant NOVX expression or activity		QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472
XX	e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial		Db	1399	GTVVWRCRRGRRDPPMSLRTVAL	1423
XX	asthma. The products of the invention can be used for gene therapy or in		QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472
XX	a vaccine. ABU65041-ABU65218 represent the NOVX polypeptides encoded by		Db	1399	GTVVWRCRRGRRDPPMSLRTVAL	1423
XX	ABX97008-ABX97185		QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472
XX	Sequence 1423 AA;		Db	1399	GTVVWRCRRGRRDPPMSLRTVAL	1423
XX	Query Match	95.6%;	QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472
XX	Best Local Similarity	91.5%;	Db	1399	GTVVWRCRRGRRDPPMSLRTVAL	1423
XX	Matches 462; Conservative	1;	QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472
XX	Matches 38; Indels	4;	Db	1399	GTVVWRCRRGRRDPPMSLRTVAL	1423
XX	Matches 4;		QY	448	GTVVWRCRRGRRDPPMSLRTVAL	472

PR	07-JUN-2002;	2002US-0386701P.	CC	encoding genes, sequences that are at least 95% identical to these or
PR	07-JUN-2002;	2002US-0386796P.	CC	sequences comprising one or more conservative substitutions in these. The
PR	07-JUN-2002;	2002US-0386931P.	CC	polypeptide, polynucleotide and antibodies against the polypeptides are
PR	07-JUN-2002;	2002US-0387078P.	CC	useful in diagnosing, treating or preventing NOVX-associated disorders,
PR	07-JUN-2002;	2002US-0387081P.	CC	e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
PR	07-JUN-2002;	2002US-0387083P.	CC	diabetes, AIDS, multiple sclerosis, graft-versus-host disease,
PR	10-JUN-2002;	2002US-0387429P.	CC	Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.
PR	10-JUN-2002;	2002US-0387540P.	CC	The nucleic acids are further used as hybridization probes, in chromosome
PR	11-JUN-2002;	2002US-0387606P.	CC	mapping, tissue typing, preventive medicine, and pharmacogenomics. The
PR	11-JUN-2002;	2002US-0387610P.	CC	polypeptides are also useful as vaccines. This sequence represents an
PR	11-JUN-2002;	2002US-0387659P.	CC	example of the polypeptide of the invention.
PR	11-JUN-2002;	2002US-0387668P.	XX	
PR	11-JUN-2002;	2002US-0387696P.	SQ	Sequence 1423 AA;
PR	11-JUN-2002;	2002US-0387859P.		
PR	12-JUN-2002;	2002US-0387934P.		
PR	12-JUN-2002;	2002US-0387960P.		
PR	12-JUN-2002;	2002US-0388032P.		
PR	12-JUN-2002;	2002US-0388096P.		
PR	12-JUN-2002;	2002US-0388432P.		
PR	12-JUN-2002;	2002US-0388479P.		
PR	13-JUN-2002;	2002US-0389120P.		
PR	14-JUN-2002;	2002US-0389146P.		
PR	17-JUN-2002;	2002US-0389742P.		
PR	18-JUN-2002;	2002US-0389604P.		
PR	18-JUN-2002;	2002US-0389884P.		
PR	19-JUN-2002;	2002US-0390006P.		
PR	19-JUN-2002;	2002US-0390144P.		
PR	19-JUN-2002;	2002US-0390209P.		
PR	25-JUN-2002;	2002US-0391726P.		
PR	06-AUG-2002;	2002US-0401628P.		
PR	09-AUG-2002;	2002US-0402268P.		
PR	12-AUG-2002;	2002US-0402822P.		
PR	13-AUG-2002;	2002US-0403458P.		
PR	15-AUG-2002;	2002US-0403617P.		
PR	15-AUG-2002;	2002US-0403732P.		
PR	26-AUG-2002;	2002US-0406182P.		
PR	12-SEP-2002;	2002US-0410085P.		
PR	13-SEP-2002;	2002US-0410505P.		
PR	23-SEP-2002;	2002US-0412955P.		
PR	30-SEP-2002;	2002US-0415195P.		
PR	23-OCT-2002;	2002US-0420627P.		
PR	23-OCT-2002;	2002US-0420718P.		
PR	24-OCT-2002;	2002US-0420852P.		
PR	31-OCT-2002;	2002US-0422750P.		
PR	01-NOV-2002;	2002US-0423095P.		
PR	05-NOV-2002;	2002US-0423748P.		
XX		(CURA-) CURAGEN CORP.		
XX		Alaobrook JP, Anderson DM, Baumgartner JC, Berghs C, Boldog FL;		
PI	Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;			
PI	Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;			
PI	Grosse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda R;			
PI	Khrantsov NV, Karochelle WJ, Li L, Liang H, Low K, Macdougall JR;			
PI	MacLachlan T, Malvankar UM, McQueeney K, Mezick AJ, Miller CE;			
PI	Millet I, Padigaru M, Patturajan M, Peyman JA, Qian X, Rastelli L;			
PI	Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;			
PI	Spytek KA, Stone DU, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ;			
PI	Wolenc AR, Zhong M, Zhong H;			
XX		WPI; 2004-053467/05.		
DR		N-PSDB; ADH42430.		
XX				
XX				
FT		New NOVX polypeptides and nucleic acid molecules useful for preventing or		
FT		treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,		
PT		atherosclerosis or diabetes, in chromosome mapping, tissue typing or in		
PT		pharmacogenomics.		
XX				
XX				
PS		Claim 2; SEQ ID NO 984; 1503pp; English.		
XX				
CC		The invention relates to 566 new isolated human polypeptides and their		

CC	encoding genes, sequences that are at least 95% identical to these or
CC	sequences comprising one or more conservative substitutions in these. The
CC	polypeptide, polynucleotide and antibodies against the polypeptides are
CC	useful in diagnosing, treating or preventing NOVX-associated disorders,
CC	e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
CC	diabetes, AIDS, multiple sclerosis, graft-versus-host disease,
CC	Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.
CC	The nucleic acids are further used as hybridization probes, in chromosome
CC	mapping, tissue typing, preventive medicine, and pharmacogenomics. The
CC	polypeptides are also useful as vaccines. This sequence represents an
CC	example of the polypeptide of the invention.
XX	
SQ	Sequence 1423 AA;
	Query Match 95.6%; Score 2407; DB 8; Length 1423;
	Best Local Similarity 91.5%; Pred. No. 1.6e-220;
	Matches 462; Conservative 1; Mismatches 4; Indels 38; Gaps 4;
Qy	1 MRELVGSGRYDQEDFSVVLQPPFQNTQLPVL----- 32
Db	924 MRELVGSGRYDQEDFSVVLQPPFQNTQLPVLQDGLPDTSFAPDCIHPNQKPHSQLARA 983
Qy	33 ----ALEPLGSKTETDLRAEMPTCTQNEPFLTRPNSNYTYPIKPAIENWGSDFLCT 88
Db	984 LWTNMLEPLGSKTETDLRAEMPTCTQNEPFLTRPNSNYTYPIKPAIENWGSDFLCT 1043
Qy	89 EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSIGDGN 148
Db	1044 EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSIGDGN 1103
Qy	149 LETHHTLPDLKXFNPKFLLGFTSTWEGTAGLNVAAEGARADMPAQAWDLVERMKNSP- 207
Db	1104 LETHHTLPDLKXFNPKFLLGFTSTWEGTAGLNVAAEGARADMPAQAWDLVERMKNSPQ 1163
Qy	208 DINLEKDWKLVTLFIGVNDLCHYCENPEAHATEYVQHIQOALDILSEELPRAFNVVV 267
Db	1164 DINLEKDWKLVTLFIGVNDLCHYCENP-----VGEYVQHIQOALDILSEELPRAFNVVV 1219
Qy	268 MELASLYQGQGGKCMALAAQNCTCLRHSSOSSEKQELKKNVNNLQHGISFSYWHQY 327
Db	1220 MELASLYQGQGGKCMALAAQNCTCLRHSSOSSEKQELKKNVNNLQHGISFSYWHQY 1279
Qy	328 REDFAVVVQPPFQNTLTPLNERGDTLTFFSEDCFHFSDRGHAEAMATLANNMLEPVGRK 387
Db	1280 REDFAVVVQPPFQNTLTPLN-RGDTLTFFSEDCFHFSDRGHAEAMATLANNMLEPVGRK 1338
Qy	388 TTSNNFTHSRALKKCPSPESPPLYTLTNRSLLPDQAEAEPEVLYWAVPAAGVGLVVGII 447
Db	1339 TTSNNFTHSRALKKCPSPESPPLYTLTNRSLLPDQAEAEPEVLYWAVPAAGVGLVVGII 1398
Qy	448 GTVVWRCRRGRRDDPPMSLRTVAL 472
Db	1399 GTVVWRCRRGRRDDPPMSLRTVAL 1423
	RESULT 8
	ADN61817
ID	ADN61817 standard; protein; 1423 AA.
XX	ADN61817;
XX	01-JUL-2004 (first entry)
XX	Human novel protein NOV24C.
XX	
KW	Human; NOVX; diabetes; obesity; infectious disease; anorexia;
KW	cancer-associated cachexia; cancer; neurodegenerative disorder;
KW	Alzheimer's disease; Parkinson's disease; immune disorder;
KW	haematopoietic disorder; dyslipidaemia; chronic disease.
OS	Homo sapiens.
XX	
PN	US2004043382-A1.

XX	Sequence 1423 AA;	94.8%;	Score 2387;	DB 8;	Length 1423;
SQ		Best Local Similarity 91.1%;	Pred. No. 1.3e-216;		

XX	Sequence 1423 AA;	94.98;	Score 2387;	DB 8;	Length 1423;
SQ		91.14;	Pred. No. 1.3e-218;		
		Best Local Similarity			
		Query Match			

Matches 460; Conservative 1; Mismatches 6; Indels 38; Gaps 4;	
QY 1	MRELVGSGRYDTQEDFSVVLQPFQNIQLPVLIA-----33
Db 924	MRELVGSGRYDTQEDFSVVLQPFQNIQLPVLQDGLPDTSFAPDCIHPNQKPHSOLARA 983
QY 34	-----LEPLGSKTETLDLRAEMPITCPTQNPFFLTPRNSNYTPIKPAIENWGSDFLCT 88
Db 984	LWTNNLEPLGSKTETLDLRAEMPITCPTQNPFFLTPRNSNYTPIKPAIENWGSDFLCT 1043
QY 89	EWKASNSVPTS VHOLRPADIKVVAALGDSLTTAVGARNSSDLPTSWRGLSWSITGGDGN 148
Db 1044	EWKASNSVPTS VHOLRPADIKVVAALGDSLTTAVGARNSSDLPTSWRGLSWSITGGDGN 1103
QY 149	LETHHTLLPNILKKNPYLLGFSTSTWECTAGLNVAAGCARADMPAQAWDLVERMKNSP- 207
Db 1104	LETHHTLLPDILKKNPNYLLGFSTSTWECTAGLNVAAGCARADMPAQAWDLVERMKNSPQ 1163
QY 208	DINLEKDWKLVTLFIGVNDLCHYCENPEAHILATEYVQHIQALDILSEELPRAFNVVVEV 267
Db 1164	DINLEKDWKLVTLFIGVNDLCHYCENP-----VGEYVQHIQALDILSEELPRAFNVVVEV 1219
QY 268	MELASLYQGQGGKCAMLAQNNCTCLRHSSQSSLEKQELKYNWNLQHGSISSFSYWHQYTO 327
Db 1220	MELASLYQGQGGKCAMLAQNNCTCLRHSSQSSLEKQELKYNWNLQHGSISSFSYWHQYTO 1279
QY 328	REDFAVVVQPFQNTLTPLNERRGDTDLTFSEDCFHFSDRGHAEMALWNNMLPEVGRK 387
Db 1280	REDFAVVVQPFQNTLTPLN- RGTDLTFSEDCFHFSDRGHAEMALWNNMLPEVGRK 1338
QY 388	TTSNFTHSRAKLKCPSPESPLYTLNRSRLLPQAEAPVLYWVPAAGVGLVVGII 447
Db 1339	TTSNFTHSRAKLKCPSPESPLYTLNRSRLLPQAEAPVLYWVPAAGVGLVVGII 1398
QY 448	GTVWVRGRRGRRDDPPMSLRTVAL 472
Db 1399	GTVWVRGRRGRRDDPPMSLRTVAL 1423
RESULT 9	
ABU65081 standard; protein; 1419 AA.	
ID	ABU65081
XX	AC
XX	ABU65081;
DT	20-MAY-2003 (first entry)
XX	Human NOV24a protein.
DE	NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;
KW	hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;
KW	human.
XX	Homo sapiens.
OS	WO200272757-A2.
XX	19-SEP-2002.
XX	08-MAR-2002; 2002WO-US006908.
XX	08-MAR-2001; 2001US-0274101P.
PR	08-MAR-2001; 2001US-0274194P.
PR	08-MAR-2001; 2001US-0274281P.
PR	08-MAR-2001; 2001US-0274322P.
PR	09-MAR-2001; 2001US-0274322P.
PR	12-MAR-2001; 2001US-0274849P.
PR	13-MAR-2001; 2001US-0275235P.
PR	13-MAR-2001; 2001US-0275578P.
PR	13-MAR-2001; 2001US-0275579P.
PR	13-MAR-2001; 2001US-0275601P.
PR	14-MAR-2001; 2001US-0276000P.
PR	16-MAR-2001; 2001US-0276776P.
PR	19-MAR-2001; 2001US-0276994P.

PR 20-MAR-2001; 2001US-0277239P.	PR 20-MAR-2001; 2001US-0277321P.
PR 20-MAR-2001; 2001US-0277321P.	PR 21-MAR-2001; 2001US-0277791P.
PR 21-MAR-2001; 2001US-0277791P.	PR 22-MAR-2001; 2001US-0277833P.
PR 23-MAR-2001; 2001US-0278152P.	PR 26-MAR-2001; 2001US-0278894P.
PR 27-MAR-2001; 2001US-0278999P.	PR 27-MAR-2001; 2001US-0279036P.
PR 28-MAR-2001; 2001US-0279344P.	PR 30-MAR-2001; 2001US-0277338P.
PR 30-MAR-2001; 2001US-0279995P.	PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.	PR 02-APR-2001; 2001US-0280900P.
PR 04-APR-2001; 2001US-0281194P.	PR 13-APR-2001; 2001US-0283675P.
PR 30-APR-2001; 2001US-0287424P.	PR 02-MAY-2001; 2001US-0288066P.
PR 03-MAY-2001; 2001US-0288342P.	PR 03-MAY-2001; 2001US-0288528P.
PR 15-MAY-2001; 2001US-0291190P.	PR 16-MAY-2001; 2001US-0291099P.
PR 16-MAY-2001; 2001US-0291240P.	PR 30-MAY-2001; 2001US-029485P.
PR 31-MAY-2001; 2001US-0294889P.	PR 31-MAY-2001; 2001US-0294899P.
PR 18-JUN-2001; 2001US-0299027P.	PR 19-JUN-2001; 2001US-0299303P.
PR 19-JUN-2001; 2001US-0299310P.	PR 10-JUL-2001; 2001US-0304354P.
PR 31-JUL-2001; 2001US-0309198P.	PR 16-AUG-2001; 2001US-0312903P.
PR 10-SEP-2001; 2001US-0318462P.	PR 12-SEP-2001; 2001US-0318770P.
PR 27-SEP-2001; 2001US-0325681P.	PR 18-OCT-2001; 2001US-0330380P.
PR 31-OCT-2001; 2001US-0335301P.	PR 14-NOV-2001; 2001US-0332172P.
PR 14-NOV-2001; 2001US-0332272P.	PR 14-NOV-2001; 2001US-0333184P.
PR 14-NOV-2001; 2001US-0333272P.	PR 21-NOV-2001; 2001US-0332094P.
PR 03-DEC-2001; 2001US-0337426P.	PR 03-DEC-2001; 2001US-0338092P.
PR 04-DEC-2001; 2001US-0337185P.	PR 03-JAN-2002; 2002US-0345705P.
PR 07-MAR-2002; 2002US-00092900.	

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Patturajan M, Gangolli E, Vernet CAM, Guo X, Tchernev V;
Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobrook JP;
Lepley DW, Rieger DK;
WPI; 2002-723332/78.
N-PSDB; ABX97048.

NOVX polypeptides and polynucleotides, useful for preventing or treating
a disorder associated with aberrant NOVX expression or activity e.g.,
cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
asthma.

Claim 1; Page 168-169; 1103pp; English.

This invention describes novel human NOVX polypeptides which have
cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive

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CC activity. Pharmaceutical compositions comprising the NOVX proteins or
CC nucleic acid molecules or NOVX antibodies are useful for preventing or
CC treating a disorder associated with aberrant NOVX expression or activity
CC e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
CC asthma. The products of the invention can be used for gene therapy or in
CC a vaccine. ABU5041-ABU6218 represent the NOVX polypeptides encoded by
CC ABX97008-ABX97185
XX
SQ Sequence 1419 AA;
Query Match 92.8%; Score 2336.5; DB 5; Length 1419;
Best Local Similarity 89.1%; Pred. No. 9.2e-214;
Matches 450; Conservative 8; Mismatches 8; Indels 39; Gaps 5;
QY 1 MRELVGSGRYDQDFSVLQPFQNIQLPVL----- 32
Db 921 MRELVGSGRYDQDFSVLQPFQNIQLPVL----- 32
QY 33 ----ALPLGSKTETDLRAEMPTCTONEPELRTPRNSNYTIPIKPAIENWGSDFLCT 88
Db 981 LWTNKLPLGSKTETDLRAEMPTCTONEPELRTPRNSNYTIPIKPAIENWGSDFLCT 1040
QY 89 EWKASNSVPTSVHQLRPADIKVVAALGDSLTAVGAPNNSSDLPTSWRGLSWISIGDGN 148
Db 1041 EWKASNSVPTSVHQLRPADIKVVAALGDSLTAVGAPNNSSDLPTSWRGLSWISIGDGN 1100
QY 149 LETHTLNLIKKNPVLIGSTSTWGTAGLNVAEGARA-RDMPAQAWDLVERMKNSP 207
Db 1101 LETHTLNLIKKNPVLIGSTSTWGTAGLNVAEGARA-RDMPAQAWDLVERMKNSP 1160
QY 208 DINLEKDWKLVTLFGVNDLCHYCENPEAHLATYVHOIQALDILSEELPRAFNVVVEV 267
Db 1161 -IHFQEDWKIITLFIGGNDLCOFND-----LVGEYVQHIQALDILSEELPRAFNVVVEV 1215
QY 268 MELASLYQGGQKCAMLAQNCTCLRHSQSLSKEQLKKNWNLQHGISFSFYHQTQ 327
Db 1216 MELASLYQGGQKCAMLAQNCTCLRHSQSLSKEQLKKNWNLQHGISFSFYHQTQ 1275
QY 328 RDEFAVVQPFQNTLTLPLNREGDITLFFSDECFHFSDRGHAEMALNWNMLEPVGK 387
Db 1276 RDEFAVVQPFQNTLTLPLN-RGDTDLTFFSDECFHFSDRGHAEMALNWNMLEPVGK 1334
QY 388 TTSNNTHSRALKCPSPSPVLYTLNRSLLPDQAEAPVLYWAVEVAAAGVLVVGII 447
Db 1335 TTSNNTHSRALKCPSPSPVLYTLNRSLLPDQAEAPVLYWAVEVAAAGVLVVGII 1394
QY 448 GTVWRCRRGRRDPPMSLRITVAL 472
Db 1395 GTVWRCRRGRRDPPMSLRITVAL 1419
RESULT 10
ADH42427
ID ADH42427 standard; protein; 1419 AA.
XX
AC ADH42427;
XX
DT 25-MAR-2004 (first entry)
XX
DE Novel human protein NOV65b.
XX
KW cardiovascular; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
KW antidiabetic; immunosuppressive; anti-HIV; neuroprotective; nootropic;
KW antiparkinsonian; antisthmatic; antifertility; cardiomyopathy;
KW atherosclerosis; hypertension; cancer; obesity; diabetes; AIDS;
KW multiple sclerosis; graft-versus-host disease; Alzheimer's disease;
KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;
KW tissue typing; preventive medicine; pharmacogenomic; vaccine.
XX
OS Homo sapiens.
XX
FN WO2003102159-A2.
XX

PD 11-DEC-2003.
XX
PF 04-JUN-2003; 2003WO-US017573.
XX
PR 04-JUN-2002; 2002US-0385490P.
PR 04-JUN-2002; 2002US-0385615P.
PR 04-JUN-2002; 2002US-0385755P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386355P.
PR 06-JUN-2002; 2002US-0386357P.
PR 06-JUN-2002; 2002US-0386447P.
PR 06-JUN-2002; 2002US-0386459P.
PR 06-JUN-2002; 2002US-0386465P.
PR 06-JUN-2002; 2002US-0386864P.
PR 07-JUN-2002; 2002US-0386701P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0387078P.
PR 07-JUN-2002; 2002US-0387081P.
PR 07-JUN-2002; 2002US-0387083P.
PR 10-JUN-2002; 2002US-0387429P.
PR 10-JUN-2002; 2002US-0387540P.
PR 10-JUN-2002; 2002US-0387866P.
PR 11-JUN-2002; 2002US-0387606P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387659P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 12-JUN-2002; 2002US-0388432P.
PR 12-JUN-2002; 2002US-0388479P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389604P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-039006P.
PR 19-JUN-2002; 2002US-0390144P.
PR 19-JUN-2002; 2002US-0390209P.
PR 19-JUN-2002; 2002US-0391728P.
PR 25-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402268P.
PR 13-AUG-2002; 2002US-0402822P.
PR 13-AUG-2002; 2002US-0403458P.
PR 15-AUG-2002; 2002US-0403617P.
PR 15-AUG-2002; 2002US-0403732P.
PR 26-AUG-2002; 2002US-0406182P.
PR 12-SEP-2002; 2002US-0410085P.
PR 23-SEP-2002; 2002US-0410505P.
PR 30-SEP-2002; 2002US-0412955P.
PR 23-OCT-2002; 2002US-0415195P.
PR 23-OCT-2002; 2002US-0420627P.
PR 23-OCT-2002; 2002US-0420718P.
PR 24-OCT-2002; 2002US-0420852P.
PR 31-OCT-2002; 2002US-0422750P.
PR 01-NOV-2002; 2002US-0423095P.
PR 05-NOV-2002; 2002US-0423748P.
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Alsebrook JP, Anderson DM, Baumgartner JC, Berghs C, Boldog FL;
Burgess CB, Casman SJ, Catterton E, Dhanabal M, Edinger SR;
Ellerman K, Ettenberg S, Gangoli EA, Gerlach VL, Gorman L;
Grosse WM, Gunther E, Guo X, Gusev VI, Herrmann JL, Ji W, Kekuda R;
Khrantsov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR;
Maclachlan T, Malyankar UM, McQueeney K, Mezick AJ, Miller CE;
Millet I, Padigaru M, Patturajan M, Peyman JA, Qian X, Rastelli L;
Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;
PI

PI Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ;
PI Wolenc AR, Zhong M, Zhong H;
XX WPI; 2004-053467/05.
DR N-PSDB; ADH42426.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, in chromosome mapping, tissue typing or in
PT pharmacogenomics.
XX
PS Claim 2; SEQ ID NO 980; 1503pp; English.
XX
CC The invention relates to 566 new isolated human polypeptides and their
CC encoding genes, sequences that are at least 95% identical to these or
CC sequences comprising one or more conservative substitutions in these. The
CC polypeptide, polynucleotide and antibodies against the polypeptides are
CC useful in diagnosing, treating or preventing NOVX-associated disorders,
CC e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
CC diabetes, AIDS, multiple sclerosis, graft-versus-host disease,
CC Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.
CC The nucleic acids are further used as hybridization probes, in chromosome
CC mapping, tissue typing, preventive medicine, and pharmacogenomics. The
CC polypeptides are also useful as vaccines. This sequence represents an
CC example of the polypeptide of the invention.
XX
SQ Sequence 1419 AA;
Query Match 92.8%; Score 2336.5; DB 8; Length 1419;
Best Local Similarity 89.1%; Pred. No. 9.2e-214;
Matches 450; Conservative 8; Mismatches 8; Indels 39; Gaps 5;
QY 1 MRELVGSGRYDTQEDFSVVLQFPFQNIQLPVL-----32
Db 921 MRELVGSGRYDTQEDFSVVLQFPFQNIQLPVLQGLPDTSPFAPDCHPNQKFSQLARA 980
QY 33 ----ALEPLGSKTETDLRAEMPTICTQNEPFLTRPNNSYTYPIKPAIENWGSDFLCT 88
Db 981 LWTNMLEPLGSKTETDLRAEMPTICTQNEPFLTRPNNSYTYPIKPAIENWGSDFLCT 1040
QY 89 EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARNSSDLPTSWRGLSWSIGGDN 148
Db 1041 EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARNSSDLPTSWRGLSWSIGGDN 1100
QY 149 LETHTLPLNLIKFNYPYLLGFSTSTWECTAGLNVAAGARA-RDMPAQAWDLVERMKNSP 207
Db 1101 LETHTLPLNLIKFNYPYLLGFSTSTWECTAGLNVAAGARARRDMPAQAWDLVERMKNSP 1160
QY 208 DINLEKQWVTLTIFGVNDLCHYCENPEAHATEYVQHIQQALDILSEELPRAFNVVVEV 267
Db 1161 -IHFQEDWKIITLPIGGNDLDFCND----LVGEYVQHIQQALDILSEELPRAFNVVVEV 1215
QY 268 MELASLYQGCGKCAMLAQNNCTCLRHSSQSLSEKQELKKNVNLQHGISSFSYWHQYTO 327
Db 1216 MELASLYQGCGKCAMLAQNNCTCLRHSSQSLSEKQELKKNVNLQHGISSFSYWHQYTO 1275
QY 328 REDFAVVVQPFQNTLPLNREGDTDLTFPSEDCFHFSDRGHAEMALWNMLEPVGK 387
Db 1276 REDFAVVVQPFQNTLPLN-RGDTDLTFPSEDCFHFSDRGHAEMALWNMLEPVGK 1334
QY 388 TTSNNFTHSRAKLKCPSPESPYLTLNRLLPQAEAEPEVLVWVPAAGVGLVVGII 447
Db 1335 TTSNNFTHSRAKLKCPSPESPYLTLNRLLPQAEAEPEVLVWVPAAGVGLVVGII 1394
QY 448 GTVWVRCRGRRDDPPMSLRTVAL 472
Db 1395 GTVWVRCRGRRDDPPMSLRTVAL 1419

RESULT 11
ADN61813
ID ADN61813 standard; protein; 1419 AA.
XX

AC ADN61813;
XX 01-JUL-2004 (first entry)
DT Human novel protein NOV24a.
DE
XX Human; NOVX; diabetes; obesity; infectious disease; anorexia;
KW cancer-associated cachexia; cancer; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; chronic disease.
XX
OS Homo sapiens.
XX
XX US2004043382-A1.
XX 04-MAR-2004.
XX
XX 07-MAR-2002; 2002US-00092900.
XX 08-MAR-2001; 2001US-0274191P.
XX 08-MAR-2001; 2001US-0274194P.
XX 08-MAR-2001; 2001US-0274281P.
XX 08-MAR-2001; 2001US-0274322P.
XX 09-MAR-2001; 2001US-0274849P.
XX 12-MAR-2001; 2001US-0275235P.
XX 13-MAR-2001; 2001US-0275578P.
XX 13-MAR-2001; 2001US-0275601P.
XX 14-MAR-2001; 2001US-0276000P.
XX 16-MAR-2001; 2001US-0276776P.
XX 19-MAR-2001; 2001US-0276994P.
XX 20-MAR-2001; 2001US-0277239P.
XX 20-MAR-2001; 2001US-0277321P.
XX 20-MAR-2001; 2001US-0277327P.
XX 20-MAR-2001; 2001US-0277338P.
XX 21-MAR-2001; 2001US-0277919P.
XX 22-MAR-2001; 2001US-0277833P.
XX 23-MAR-2001; 2001US-0278152P.
XX 26-MAR-2001; 2001US-0278894P.
XX 27-MAR-2001; 2001US-0278999P.
XX 27-MAR-2001; 2001US-0279036P.
XX 28-MAR-2001; 2001US-0279344P.
XX 30-MAR-2001; 2001US-0279995P.
XX 30-MAR-2001; 2001US-0280233P.
XX 02-APR-2001; 2001US-0280802P.
XX 02-APR-2001; 2001US-0280822P.
XX 02-APR-2001; 2001US-0280900P.
XX 04-APR-2001; 2001US-0281444P.
XX 13-APR-2001; 2001US-0283675P.
XX 30-APR-2001; 2001US-0287424P.
XX 02-MAY-2001; 2001US-0288066P.
XX 03-MAY-2001; 2001US-0288342P.
XX 03-MAY-2001; 2001US-0288528P.
XX 15-MAY-2001; 2001US-0291190P.
XX 16-MAY-2001; 2001US-0291099P.
XX 16-MAY-2001; 2001US-0291240P.
XX 30-MAY-2001; 2001US-0294485P.
XX 31-MAY-2001; 2001US-0294899P.
XX 31-MAY-2001; 2001US-0294899P.
XX 18-JUN-2001; 2001US-0299027P.
XX 19-JUN-2001; 2001US-0299303P.
XX 19-JUN-2001; 2001US-0299310P.
XX 10-JUL-2001; 2001US-0304354P.
XX 31-JUL-2001; 2001US-0309198P.
XX 16-AUG-2001; 2001US-0312903P.
XX 10-SEP-2001; 2001US-0318462P.
XX 12-SEP-2001; 2001US-0318770P.
XX 27-SEP-2001; 2001US-0325430P.
XX 27-SEP-2001; 2001US-0325681P.
XX 18-OCT-2001; 2001US-0330380P.
XX 31-OCT-2001; 2001US-0335301P.
XX 14-NOV-2001; 2001US-0332172P.
XX 14-NOV-2001; 2001US-0332271P.

immunological disorder; scleroderma; systemic lupus erythematosus; allergy; gastrointestinal disorder; Crohn's disease; renal disorder; Goodpasture's syndrome; infection; viral; bacterial; fungal; parasitic; protozoal; helminthic; cardiovascular disorder; atherosclerosis; hepatic disease; cirrhosis; transgenic animal; human.

Homo sapiens.

WO2004044165-A2.

27-MAY-2004.

10-NOV-2003; 2003WO-US035946.

13-NOV-2002; 2002US-0426105P.

12-DEC-2002; 2002US-0433215P.

07-MAR-2003; 2003US-0453127P.

13-MAR-2003; 2003US-0454801P.

24-APR-2003; 2003US-0454959P.

24-APR-2003; 2003US-045619P.

01-AUG-2003; 2003US-0491800P.

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Lee SY, Marquis JP, Murege J, Swarnakar A, Yang YG,

WPI; 2004-420307/39.

N-PSDB; ADO18836.

New LIPAM polypeptides, useful for diagnosing, preventing, and treating disorders associated with abnormal expression or activity of LIPAM, e.g. neuromuscular, immunological, cardiovascular disorders, cancer and/or infections.

Claim 1; SEQ ID NO 10; 207pp; English.

This invention relates to novel human lipid-associated molecules (LIPAM) and the DNA sequences which encode them. The invention may be useful for the production of compounds with a neuroprotective, relaxant, antithyroid, antidiabetic, cytostatic, dermatological, immunosuppressive, antiinflammatory, thymomimetic, antiallergic, cerebroprotective, gastrointestinal, hepatotropic, nephrotropic, anticonvulsant, antiparkinsonian, antibacterial, antiparasitic, fungicide, protozoacide, virucide, uropathic, antirheumatic, cardiant, cardiovascular, anti-HIV or neurotropic activity acting as LIPAM agonists or antagonists. In addition, the disclosed sequences may be useful for gene therapy. The invention may be useful for diagnosing, preventing, and treating disorders associated with an abnormal expression or activity of LIPAM, such as neurodegenerative disorders (for example Parkinson's disease, Alzheimer's disease), muscular disorders (for example myotonic dystrophy, catatonias), endocrine disorders (for example diabetes, Grave's disease), cancers (for example leukaemia, cervical or breast cancers), immunological disorders (for example scleroderma, systemic lupus erythematosus, allergies), gastrointestinal disorders (for example Crohn's disease), renal disorders (for example Goodpasture's syndrome), infections (for example viral, bacterial, fungal, parasitic, protozoal, helminthic), cardiovascular disorders (for example atherosclerosis), or hepatic diseases (for example cirrhosis). LIPAM or its fragments may also be used in screening for compounds that specifically bind to and modulate the activity of LIPAM. The polynucleotides can be used to create humanised animals or transgenic animals to model human disease. The present sequence is that of a human lipid-associated molecule (LIPAM) protein of the invention.

Sequence 1433 AA;

Query Match 92.7%; Score 2334.5; DB 8; Length 1433;
Best Local Similarity 88.7%; Pred. No. 1.5e-213;
Matches 447; Conservative 0; Mismatches 0; Indels 57; Gaps 2;

1 MRELVGSGRYDTQEDFSVVLQPPFQNTQLPVLADGLPDTSPFAPDCHPNKQFHSQLARA 33
|||||

Db	955	MRELVGSGRYDTQEDFSVVLQPPFQNTQLPVLADGLPDTSPFAPDCHPNKQFHSQLARA	1014
Qy	34	-----LEPLGSKTETLDRAEMPTTCTQNEPFLRTPRNSNYTYPPIKPAIENWGSDFLCT	88
Db	1015	LWTNMLEPLGSKTETLDRAEMPTTCTQNEPFLRTPRNSNYTYPPIKPAIENWGSDFLCT	1074
Qy	89	EWKASNSVPTSVHQLRPADIKVVAALGDSLTAVGARPNNSDDLPTSWRGLSWSIGDGN	148
Db	1075	EWKASNSVPTSVHQLRPADIKVVAALGDSLTAVGARPNNSDDLPTSWRGLSWSIGDGN	1134
Qy	149	LEHTHTLPTNLTKKFNPYLLGFSTWEGTAGLVAAEGARADMPAQAWDLVERMKNSPD	208
Db	1135	LEHTHTLPTNLTKKFNPYLLGFSTWEGTAGLVAAEGARADMPAQAWDLVERMKNSPD	1194
Qy	209	INLEKDWKLVTLFIGVNDLCHYCENPEAHILATEYVQHIQQALDILSELPRAFVNVVEVM	268
Db	1195	INLEKDWKLVTLFIGVNDLCHYCENPEAHILATEYVQHIQQALDILSELPRAFVNVVEVM	1254
Qy	269	ELASLYQGQGGKCAMLAQNNCTCLRHSQSLSLEKQELKKNVNNLOHGISSFSYWHQYTOR	328
Db	1255	ELASLYQGQGGKCAMLAQNNCTCLRHSQSLSLEKQELKKNVNNLOHGISSFSYWHQYTOR	1314
Qy	329	EDFAVVVQPPFQNTLTPLNERGDTDLTFSEDCFHFSRDRGHAENAIALWNNMLSPVGRKT	388
Db	1315	EDFAVVVQPPFQNTLTPLNERGDTDLTFSEDCFHFSRDRGHAENAIALWNNMLSPVGRKT	1366
Qy	389	TSNNFTHSRACLKCPSPESPLYTLRNSRLLPDQAEAPVLYWAVPVAAGVGLVVGIIIG	448
Db	1367	-----ESPPLYTLRNSRLLPDQAEAPVLYWAVPVAAGVGLVVGIIIG	1409
Qy	449	TVVMCRGRRGRRDPPMSLRVAL	472
Db	1410	TVVMCRGRRGRRDPPMSLRVAL	1433
RESULT 13			
AAW30751			
ID	AAW30751	standard; protein; 1450 AA.	
AC	AAW30751;		
XX	28-JAN-1998	(first entry)	
DT			
DE		Rat phospholipase-B/lipase.	
XX			
XX		phospholipase B; lipase; supplement; pancreatic phospholipase; reagent; screening, rat.	
XX			
OS		Rattus rattus.	
XX			
XX		Location/Qualifiers	
FT	Key	1. .30	
FT	Peptide	/label= signal_peptide	
FT	Protein	31	
FT	Region	/label= mature_protein	
FT	Region	43. .652	
FT	Region	/label= repeat_region_1	
FT	Region	367. .712	
FT	Region	/label= repeat_region_2	
FT	Region	714. .1059	
FT	Region	/label= repeat_region_3	
FT	Region	1070. .1408	
FT	Region	/label= repeat_region_4	
FT	Domain	1421. .1443	
FT		/label= transmembrane_binding_domain	
XX			
PN	JP09248190-A.		
XX			
PD	22-SEP-1997.		
XX			
PF	15-MAR-1996;	96JP-00086022.	
XX	15-MAR-1996;	96JP-00086022.	
PR			

QY	129	SSDLPTSWRGLSWISGGDGNLTHTTLPNLKKNFNPYLLGFSTSTWEGTAGLNVAEGAR	200
Db	141	SSDLPTSWRGLSWISGGDGNLTHTTLPNLKKNFNPYLLGFSTSTWEGTAGLNVAEGAR	200
QY	189	ARDMPAQAWDLVERMKNSPDINLEKDWKLVTLLFIGVNDLCHYCENPEAHLATEYVVOHIQ	248
Db	201	ARDMPAQAWDLVERMKNSPDINLEKDWKLVTLLFIGVNDLCHYCENPEAHLATEYVVOHIQ	260
QY	249	ALDILSE 255	
Db	261	ALDILSE 267	
RESULT 15			
ABBI1053	ID	ABBI1053 standard; peptide; 267 AA.	
XX	AC	ABBI1053;	
XX	DT	11-JAN-2002 (first entry)	
XX	DE	Human phospholipase B homologue, SEQ ID NO:1423.	
XX	KW	Human; cytokine; cell proliferation; cell differentiation; growth factor;	
KW	KW	haematopoiesis regulation; tissue growth; immunomodulator; activin;	
KW	KW	inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;	
KW	KW	proliferation; metastasis; cancer; tumour; haematopoietic disorder;	
KW	KW	myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;	
KW	KW	chronic inflammatory condition; proliferative retinopathy;	
KW	KW	atherosclerosis; coronary heart disease; arterial ischaemia;	
KW	KW	bone disorder; osteoporosis; vascular growth disorder;	
KW	KW	tissue regeneration; wound healing; infection; immune disorder;	
KW	KW	cell culture; drug screening; gene therapy; antiinflammatory;	
KW	KW	antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;	
KW	KW	cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;	
KW	KW	antifungal; vulnary; antiulcer.	
OS		Homo sapiens.	
XX	PN	WO200157188-A2.	
XX	PD	09-AUG-2001.	
XX	PF	05-FEB-2001; 2001WO-US003800.	
XX	PR	03-FEB-2000; 2000US-00496914.	
XX	PR	27-APR-2000; 2000US-00560875.	
XX	PA	(HYSE-) HYSEQ INC.	
XX	PI	Tang YT, Liu C, Drmanac RT;	
XX	DR	WPI; 2001-457740/49.	
DR	N-PSDB:	ABA08297.	

differentiation activities; stem cell growth factor activity;
haematopoiesis regulatory activity; tissue growth activity;
immunomodulatory activity; activin- or inhibin-related activities;
chemotactic or chemokinetic activities; haemostatic, thrombotic or
thrombolytic activities; receptor or ligand activities; or may be
involved in oncogenesis, cancer cell proliferation or metastasis.
Depending on their biological activities, polypeptides and nucleotides of
the invention are useful for preventing, treating or ameliorating medical
conditions, e.g., by protein or gene therapy. Such conditions include
cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
proliferative retinopathy, atherosclerosis, coronary heart disease,
arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
vascular growth. Polypeptides involved with tissue regeneration and
repair (or nucleic acids encoding them) may be used to promote wound
healing (e.g., of burns, incisions and ulcers), while those with
immunomodulatory activities may be used in the treatment of viral,
bacterial and fungal infections in addition to immune disorders.
Polypeptides with growth factor activity may be used in cell cultures to
promote cell growth. For example, such polypeptides may be used to
manipulate stem cells in culture to give rise to neuroepithelial cells
that can be used to augment or replace cells damaged by illness,
autoimmune disease or accidental damage. The polypeptides and nucleotides
may also be used in the diagnosis of the above conditions, and in drug
screening techniques. The present sequence represents a novel human
polypeptide of the invention

Sequence 267 AA;

Search completed: March 25, 2005, 14:33:16
Job time : 180 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 25, 2005, 14:27:54 ; Search time 48 Seconds
(without alignments)
734.049 Million cell updates/sec

Title: US-09-778-961-2

Perfect score: 2518

Sequence: 1 MRELVGSGRYDTQEDFSVL.....RCRRGGRDPPMSLRITVAL 472

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCUTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	336.5	13.4	215	4	US-09-270-767-44304
2	160.5	6.4	107	4	US-09-270-767-59726
3	110.5	4.4	921	4	US-09-248-796A-14950
4	100	4.0	866	3	US-09-040-843-2
5	100	4.0	866	3	US-09-621-855-2
6	98.5	3.9	458	4	US-09-800-170-3
7	98.5	3.9	863	2	US-08-668-271-2
8	98	3.9	293	4	US-09-252-991A-27435
9	97.5	3.9	640	4	US-09-336-115C-14
10	94.5	3.8	482	3	US-09-189-129-2
11	94.5	3.8	482	4	US-09-824-286-2
12	94.5	3.8	672	3	US-09-040-843-4
13	94.5	3.8	672	3	US-09-621-855-4
14	94	3.7	441	4	US-09-328-352-7914
15	94	3.7	708	4	US-09-336-115C-2
16	93	3.7	798	4	US-09-203-453-5
17	93	3.7	798	4	US-09-900-236-5
18	92.5	3.7	307	4	US-09-107-532A-5252
19	92	3.7	481	4	US-09-949-016-7885
20	92	3.7	1540	4	US-09-949-016-11382
21	92	3.7	1540	4	US-09-949-016-11383
22	92	3.7	1719	2	US-08-459-568-4
23	92	3.7	1719	3	US-08-399-411-4
24	92	3.7	1719	3	US-08-516-859A-4
25	92	3.7	1719	3	US-09-586-472-4
26	92	3.7	1719	4	US-09-528-706-4
27	90	3.6	2522	3	US-09-251-645-13

ALIGNMENTS

RESULT 1

US-09-270-767-44304
; Sequence 44304, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44304
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44304

Query Match 13.4%; Score 336.5; DB 4; Length 215;
Best Local Similarity 41.7%; Pred. No. 5.8e-28;
Matches 75; Conservative 29; Mismatches 71; Indels 5; Gaps 3;

Qy	91	KASNSVPTSVHQLRPADIKVVAALGDSI--TTAVGARPNNSSDLPTSWRGLSWSIGDGNLE	150
Db	32	KRSPERTSVHRLRPGDIDVIGMGDSLTAGNGIFATNLLHVTVENRGVWVWSIGQYDWR	91
Qy	151	THHTLPNLIKFPNLYLLGFSTS---TWEGTAGLNVAAGARADMPAQAWDLVERMKNSP	207
Db	92	KYLTLPNLIKFEFNLYGYAIKDGISTDRSRFDVLAAMSRLDMPHMAKVLVRMORDP	151
Qy	208	DINLEKDKWLTLPFGVNDLC-HYCENPEAHATE-VVQHTQQALDILSEELPRAFNWV	265
Db	152	RVNMTSDWKLVTLPFGNNDFTDICYYPEPEKTVDMHERNMLKTYRYLRDNPVRLMLNIV	211

RESULT 2

US-09-270-767-59726
; Sequence 59726, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59726
; LENGTH: 107
; TYPE: PRT

ORGANISM: *Drosophila melanogaster*
 HIS-09-270-767-59726

Query Match	6.4%	Score 160.5	DB 4	Length 107
Best Local Similarity	38.0%	Pred. NO.2.7e-09		
Matches	38	Conservative 18	Mismatches 39	Indels 5
Gaps				
168	GFSTWEGTAGLVAAEGARADMPAQANDLVVERKNSPDINLEKDWKLTFLTIGVNDL	227		
QY				
	:: ::	:: ::		
7	GIST---DRSGFDVLAASMDPMMAKLVRRQDRPVNNTSDKMLTFLIGNDF	63		
DB				
228	C-HYCENPEARLATE-YVQHIQQALDILSEELPRAFVVV	265		
QY				
	:: ::	:: ::		
64	CTDICYPPEKPTVDWHERNMLKTYLRDRNPRMLNIV	103		
DB				

```

RESULT 3
US-09-248-796A-14950
; Sequence 14950, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14950
; LENGTH: 921
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-14950

```

Query Match	4.4%	Score 110.5	DB 4	Length 921		
Best Local Similarity	20.2%	Pred. No. 0.036				
Matches	94	Conservative 54	Mismatches 138	Indels 179	Gaps 25	
Qy	37	LGSKTEILDRAMPITCPTQNEPFLR	---	TPRNSNYTYPKPA	---IENWGSDFL 86	
Db	431	LSSLETTQISVS	---PDLEDFFVPSEGLFVDPEESRV	---IEDALNYIEN	---L 478	
Qy	87	CTEWKASNSVPTS VHQLRPADI	---	KVNAALGDSLTTAVGARNSSDLPTSMRG	138	
Db	479	ASQDRVSDSEFCFSAACRTASMCMLDFGGKII SLL	---	SNLP	---518	
Qy	139	LSWSICG	---DGNLEHTHTLPNLLKKF	---NPYLLGFSTWEGTAGLNVAAGARAR	190	
Db	519	-SWGPGGLKYDKNTGIRTAPEVEKKLPSADNEYKLLAREFTIEKSVGLDVHVVSHTPV	577			
Qy	191	DMPAQAW	---	DLVERMKNSPDINLEKWKLV	---LFI GWN DLCHY	---CEN-- 233
Db	578	DLSNVGWLASVTGGBITRWAN	---PDFERDGRALTAKTYNSVKNSGGYQGLKURCSNGL	634		
Qy	234	---	PEAHIAEYVQHIOQ	-ALDILSELPRAFVNVVEMELASLYOQGGKCAML	284	
Db	635	QVTQYVGTSSSIDTSIVGNIQDPIVLSBDL	---TFILL	---	YDGK-----L 679	
Qy	285	AAQNQNTCLRHSQSSL	---EKOELKKVN	-WNIQHGISSEFSYWHQVTOREDFAVVVQPFQ	340	
Db	680	SPKLDG	---HFQAALYTDPNQVRKVRVINLAVSK			
Qy	341	NLTLPNLRGDDTLTFEEDCHPFSDRGHA	---			
Db	714	---	SLEDVFFHTDENAVTTIVRDTLSFVCOQSLLLERESINNKLVD	757		
Qy	383	PVGRKTTNNFTSHRAKLKCPSPESPYLYTLRNSRLLPDQAEAP	427			
Db	759	IETHVAMNEFGHNRAK	-----TLSNKMFLFPDSLKHLF	790		

RESULT 4

```

US-09-040-843-2
; Sequence 2, Application US/09040843
; Patent No. 6124119
;
; GENERAL INFORMATION:
;
; APPLICANT: Jaworski, Deborah J.
; APPLICANT: Wang, Min
; APPLICANT: Shilling, Lisa K.
; APPLICANT: Burnham, Martin
; APPLICANT: Foshberry, Andrew
; APPLICANT: Hodgson, John E.
; APPLICANT: Lawlor, Elizabeth
; APPLICANT: Rosenberg, Martin
; APPLICANT: Ward, Judith
; TITLE OF INVENTION: MeCB
;
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Dechert, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
;
; ZIP: 19103-2793
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Diskette
;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/09/040,843
; FILING DATE:
;
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: 60/057,535
; FILING DATE: 29-AUG-1997
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Falk, Stephen T
;
; REGISTRATION NUMBER: 36,795
;
; REFERENCE/DOCKET NUMBER: GM10082
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
;
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 2:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 866 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-040-843-2

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Query Match	4.0%;	Score 100;	DB 3;	Length 866;	
Best Local Similarity	21.6%;	Pred. No. 0.45;			25;
Matches	97;	Conservative	51;	Mismatches 119;	Indels 182; Gaps
QY	106	ADIKVVAALGD---	SU--TAVGARPNSSDLPTSMRWGLSWSIGCGDNLE-----	-----THHTTL	155
DB	134	ARARVVKALGNP	EMSKNNQAQSKNNITPYLDSLARDLI--VIAKDGTLD	PVIGRDKETRV	192
QY	156	PNILK----	KENPYLLGFSTTWEGTAGLNVAAG--ARA-----	-----RMPAAQAWL--	199
DB	193	IEVLRRRTKKNPVLIG-----	EPGVGKTAIAEGLAQAIVNNEVPETLKKRKMVSLD	MGTT	246
QY	200	-----VERMKN-----	-----	-----SPDI--	209
DB	247	VVAGTKRGFEERLKKWME	EQAGNVILFIDELHTLVGAGGAECADASNILK	PALAR	306
QY	210	-----NLEKDWL-----	-----	-----VTLPFIGVNDLCHYCEN	PEA
DB	307	GELOCIGATTUDEYRKNI	EKDAALERFPQVQDESPVDTVA	ILKGLD-----	RYEA

us-09-778-961-2.ra1

Mon Mar 28 09:43:26 2005

184 AEGARDMPAQAWDLVERMKNSPDINLEK-----DWKLVTLFIGVNDL----- 227
 181 -----VPYFELLKNLTQIRELNLESVNISSTIPSNFSSHTLTTLQSLGTELHILP 232
 228 -----CHYCENPE-----AHLATEYVQHIQOALDILSELPAFVN 263
 233 ERFVHLSNLSLHLSVNPQLTVRPTTKWNSASLMTLYVDSV-----IADRIKPSF-- 285
 264 VVEMELASLYOQGGKCM-----LAAQNCTCLRHSSQSLEK-----DELKK- 307
 286 -----SHLTSLHLYMGRCNLGSGIPKPLMNLNIVFLHGDHLEGPISHFTIFEKLEL 341
 308 --VNNMLQHGISFSYWHQYTOREDFAVVVPFPQNTLT---PLNERGDTDLTFSEDCF 362
 342 SLVNNFDGGLFSLP-NTQLERLDS-----SNSLTGPIPSNISGLQNL-----ECL 388
 363 HFSDRGHAEMALMNNMPLPVGKRTTSNN-----FTHSRAKLKCPSP 406
 389 YLSS-NHLNGSIPTSWIFSLPSLVELDLNNFTSGKIQEFKSTLSAVTLKONKLGRIPN 447
 407 SPYLYTLNLSRL 419
 448 S--LNNOKNLOLL 458

RESULT 8

US-09-252-991A-27435
 ; Sequence 27435, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252.991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 27435
 ; LENGTH: 293
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-27435

Query Match 3.9%; Score 98; DB 4; Length 293;
 Best Local Similarity 24.7%; Pred. No. 0.11;
 Matches 73; Conservative 39; Mismatches 120; Indels 64; Gaps 16;

178 AGLNVAEG-----ARADMPAQAWDLVERMKNSPDINLEKDWKLVTLFIGVNDLCHYCE 232
 4 AGASFASDGHAPTLOSROKOPREFPTVSKLKHGFNLT-----TLSFNIYDIC-YAE 57
 233 NPEAHLATEYVQHIQOALDILSELPAFVNVPVMEASL-----YQGGGKCMALAA 286
 58 TPEDLQA-YVQYIDEYD--AERLTQILTDVVDDIIGANILNIAIARQDYDPOGASVTILIS 113
 287 QNNCTCLRHSSQSLEKQELKKNVNNLOHGSISSFYHQQ-----TOREDFAV--- 333
 114 EQPVT---PTDSQIESPGPLPDTLAILHLDKSHITVHTPEIHVFDGIAIFRVDIVSTC 170
 334 -VQVPPQNTLTPLNERGDTDLTF-----FSEDC---HFSDRGHAEMALMNNMLE 382
 171 GVTSPL--KALNYLIHOFDSIVTVYRVRGFTDIEGRKHFD--HEINSI---QNYLS 223
 383 PVGRK-----TTSNNFTHSRAKLKCPSPSPYLYTLNSELPPQAEAEPEVL 430
 224 DDTREAYQMTDVNVYQENLPHFTKMLIKDFELEN-YLFGDATRTLSAQREQVTERL 278

RESULT 9

392 NFTHSRAKLKCPSPSPYLYTLNRSR 417
 426 RFVYKGPVYCLTGPNNVYVQRNGK 451
 RESULT 7
 US-08-666-271-2
 ; Sequence 2, Application US/08666271
 ; Patent No. 5920000
 ; GENERAL INFORMATION:
 ; APPLICANT: JONES, JONATHAN D
 ; APPLICANT: HAMMOND-KOSACK, KIM E
 ; APPLICANT: THOMAS, COLWYN M
 ; APPLICANT: JONES, DAVID A
 ; TITLE OF INVENTION: PLANT PATHOGEN RESISTANCE GENES AND USES
 ; TITLE OF INVENTION: THEREOF
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22201
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/666.271
 ; FILING DATE: 19-SEP-1996
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB94/02812
 ; FILING DATE: 23-DEC-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9326428.1
 ; FILING DATE: 24-DEC-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9409363.0
 ; FILING DATE: 11-MAY-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SADOFF, B.J.
 ; REGISTRATION NUMBER: 36,663
 ; REFERENCE/DOCKET NUMBER: 620-7
 ; TELEPHONE: 703-816-4091
 ; TELEFAX: 703-816-4100
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 863 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-666-271-2

Query Match 3.9%; Score 98.5; DB 2; Length 863;
 Best Local Similarity 19.9%; Pred. No. 0.66;
 Matches 98; Conservative 59; Mismatches 167; Indels 169; Gaps 23;

44 LDLEAEMPTICPTQ-----NEPFLRTPRNSNYTYPIK-----PAIENWGSDFLC 87
 18 LALSSSLPHLCPEQOALSILQFKNMFTINENASDVCYDIITYVDIQSYPTLSWKNKSTSC 77
 88 TEWKASNSVPTSVHQLRADIKVVAALGDSLTAVAGARPNNSSDLPTSWRGLSWSI--- 143
 78 CSWDGVHCDETT-QGVIALDRCQLQKGFHSNLSULFQSLNKRDLISFNFTGSLISPK 136
 144 -GGDGNLETHLTPLNLIKKNPFLYLGFTSTWECTA-----GLNVA 183
 137 FGFSNL--TH-----LDLSHSFPTGLIPSEICLSKLHLVLRICDQYGLSL- 180

[illegible]

us-09-778-961-2-rai

Mon Mar 28 09:43:26 2005

Hession, Catherine A
Whitty, Adrian
TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bogen, Inc.
STREET: 14 Cambridge Center
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02142
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/824,286
FILING DATE: 02-Apr-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017,466
FILING DATE: 10-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kaplan, Warren A.
REGISTRATION NUMBER: 34,199
REFERENCE/DOCKET NUMBER: A006 PCT CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 679-2000
TELEFAX: 617 679-2838
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 482 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: YES
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-824-286-2

Query Match 3.8%; Score 94.5; DB 4; Length 482;
Best Local Similarity 20.6%; Pred. No. 0.64; Indels 125; Gaps 25;
Matches 83; Conservative 62; Mismatches 133;
QY 114 LGDSLTTAVGARPNNSSD-----LPTSWRGLSWISIGDGNLEHTTILNLIKFPN 164
Db 19 LGVGLNTTI-LTPNGNEDTTADFFLTWPTD---SLSV-----STLPLPEVQCFV 64
QY 165 YLLGFSTSTWGTAGLNVAAGARADMPAQAWDLVERMKSPDINLEKDWKLVTLFIGV 224
Db 65 ENVEYMNCTW-----NSSSE-PQPTNLTLYW-----YKNSDNDKVK-----CSHYLFS 108
QY 225 NDLCHYC--ENPEALHATYVQHIQOALDILSEELPRAFVNVVYVMEASLYQGGGKCA 282
Db 109 EITSGCQKQKEIHLHYQYVQLQPRE-----PRR--QATQMLKLNL-----V 152
QY 283 MLAAQNCTCLRHSSQSLKQELKYNWN-----LHGSSFSYV-HQYTO-----RE 329
Db 153 IPWAPENLTLLKLSQSLE-----LNWNNRFLNHCHLEHLVQYRTDHDHSWTEQSVDRH 206
QY 330 DFAVVVQFPQNTLTPLNERGDTDLTFEEDCFHFSDRGHAEMATALMNMNLEPY--GRK 387
Db 207 KFLSPVSDGQRYNFRVRSR-----FNPLC-----GSAQH-----WSEWHPHWSGN 249
QY 388 TTNNFTSHRAKLKCPSE-----SPLYX-----TLNRSR-----LLPDQAEAPVYL 430
Db 250 TSKENVKTHTCPCPAPPELLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVK 309
QY 431 Y-WAVPVAAGVLVIGLIGIVVWRCRGGRGPPMPSLRTVAL 472
Db 310 FNTYVD-----GVEVHNKTKPREEQNSTYRVVSV 340

RESULT 12
US-09-040-843-4
Sequence 4, Application US/09040843
Patent No. 6124119
GENERAL INFORMATION:
APPLICANT: Jaworski, Deborah J.
APPLICANT: Wang, Min
APPLICANT: Shilling, Lisa K.
APPLICANT: Burnham, Martin
APPLICANT: Fotherberry, Andrew
APPLICANT: Hodgson, John E.
APPLICANT: Lawlor, Elizabeth
APPLICANT: Rosenberg, Martin
APPLICANT: Ward, Judith
TITLE OF INVENTION: MecB
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,843
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/057,535
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM10082
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
TELEFAX: 215-994-2222
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 672 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-040-843-4
Query Match 3.8%; Score 94.5; DB 3; Length 672;
Best Local Similarity 21.8%; Pred. No. 1.1;
Matches 74; Conservative 44; Mismatches 103; Indels 119; Gaps 18;
QY 116 DSLTTAVGA-----RPNSSDL--PTSWRGLSWISIGD-----GNLEHTTILNLIKFPN 163
Db 133 DELHTLVGAGAGCAIDASNLIKPALARGELQICIGATTLDEYRKNIKEDAALE---RRFQ 189
QY 164 PY-----LLGFSTSTWGTAGLNVAAGARA-----RDMPAQAWDLV 200
Db 190 PVQVDESVVDVTVAIKGLGLDRDYEAHHRINISDEATEAAVKLSNRYVSDRFLPDKAIDL 249
QY 201 ERMKNSPDINLEKDWKLVTLFIGVNDLCHYCNPEALHATEYVQHIQOALDILSEELPRA 260
Db 250 D--EASSKVL-----KSHHTPNNLKEIQEIKVKNE-----280
QY 261 FVNVVMEASLYQGGGKCAMLAAQ--NNCTCLRHSSQSLKQ--ELKKVNW-NLQHI 316
Db 281 -----KDAVHAQEFENAAANLRDKQTKLEKQYEAKNFKNAQNGM 321

Qy 317 SSFSYWHQYTOREDFAVVVQFPFQNTLTPLNERGDTDLTFPSEDCFHSDRGHAEAMATL 376
Db 322 ST-----SLSEEDIAEVIAGWTGIPITKINE---TE-----SEKLSLEDTLHERV----- 364
Qy 377 WNNMLEPVGRKTTSNFT-----HSRAKLKCPSPESPPLY 411
Db 365 -----IGQKDAVNSISKAVRRARAGLKDPRPIGSPIF 397

RESULT 13

US-09-621-855-4
; Sequence 4, Application US/09621855
; Patent No. 634608
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Deborah J.
; Wang, Min
; Shilling, Lisa K.
; Burnham, Martin
; Fosberry, Andrew
; Hodgson, John E.
; Lawlor, Elizabeth
; Rosenberg, Martin
; Ward, Judith
; TITLE OF INVENTION: MecB
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert, Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2793
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/621,855
; FILING DATE: 24-Jul-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/040,843
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM10082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 672 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-621-855-4
Query Match 3.8%; Score 94.5; DB 3; Length 672;
Best Local Similarity 21.8%; Pred. No. 1.1;
Matches 74; Conservative 44; Mismatches 103; Indels 119; Gaps 18;
Qy 116 DLSLTAVGA-----RPNSSDL--PTSWRGLSWSTIGD-----GNLEHTHTLPLNLKKFN 163
Db 133 DELHTLVGAGGAIDAIDANILKPALARGELQCIGATTLDYRKNIKDAALE---RRFQ 189
Qy 164 PY-----LLGFSTSTWECTAGLVAAEGARA-----RMPAQAWDLV 200
Db 190 PVQVDEPSWDTVAILKGLRDYBAHHRINISDEAIEAAVKLSNRYVSDRFLPDKAIDLI 249

Qy 201 ERMKNSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHQIQAALDILSELPR 260
Db 250 D--EASSKVL-----KSHHTPNNLKIEIEKVKNE----- 280
Qy 261 FNVVVEVWELASLYQGQGGKCAMLAQ--NNCTCLRHSSQSLEKO-ELKKVNW-NLQHG 316
Db 281 -----KDAAVHAQEFENANLRDQTKLEKQYERAKNEWKVAQNGM 321
Qy 317 SSFSYWHQYTOREDFAVVVQFPFQNTLTPLNERGDTDLTFPSEDCFHSDRGHAEAMATL 376
Db 322 ST-----SLSEEDIAEVIAGWTGIPITKINE---TE-----SEKLSLEDTLHERV----- 364
Qy 377 WNNMLEPVGRKTTSNFT-----HSRAKLKCPSPESPPLY 411
Db 365 -----IGQKDAVNSISKAVRRARAGLKDPRPIGSPIF 397

RESULT 14

US-09-328-352-7914
; Sequence 7914, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7914
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7914

Query Match 3.7%; Score 94; DB 4; Length 441;
Best Local Similarity 20.6%; Pred. No. 0.62;
Matches 85; Conservative 52; Mismatches 146; Indels 130; Gaps 22;

Qy 5 VSGGRYDTQEDFVSVLQFPFQNIQLPVLAEPLGSKTKETLDRAMPITCTQNEPFPURT 64
Db 45 VGAG-----LLLPQ-----AGLAVFHLGVDKALTGAK--VTGLEGLPDKRL 87
Qy 65 PRNSNY-----TYPIKPAIENMGSDFLCTEWKASNSVPTSV----- 100
Db 88 LVNSHYREASTNLYGLGHRATLCHLVLTQKLSEYSSQI---TWCWNHVSFVEHNDVR 144
Qy 101 -----HQLRPADIKVVAALGDSLTAVGARNPNSSDLPTSW-----RGLSWSIGGDN 148
Db 145 IFGSHQNKQFD-----ACFDGLLIANGAR---SQLRPKAWKVDKAYPWGAWSIVP--- 193
Qy 149 LEHTHTLPLNLKPF---NPYLLG-----FSTSTWE-GTAGLVAAEGARAR 190
Db 194 -ECQVLSEILHQPYDRSKIMMGLPTGAIPTEPQRLSSVFWLSLPTQLQSFQDEQAK 252
Qy 191 DMPAQAWDLVERMKNSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHLATEYVQHQIQAAL 250
Db 253 -----QAW-LKQVSEWPKV---ADM-----LKEILYNSQTQPKWSANY-----R 289
Qy 251 DILSEELPRAPVNVV-EVMELASLYQGQGGKCAMLAQNNCTCLRHSQSSLEKOLKKVN 309
Db 290 DVVMTQFGQGRIGVIGDAAHAMSPQLGGANMALLDAWAFSQSLQHAQKN-----QNID 343
Qy 310 WNLQHGSSSYWHQYTOREDFAVVVQFPFQNTLTPLNERGDT-----TDLTF 356
Db 344 WSL-----LMQHYHQLRGSSSTQFYQLSRLLTPLYQSDDWAGGLRDLVF 388

RESULT 15

US-09-336-115C-2
; Sequence 2, Application US/09336115C
; Patent No. 6576244
; GENERAL INFORMATION:

Search completed: March 25, 2005, 14:38:13
Job time : 54 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 25, 2005, 14:36:30 ; Search time 144 Seconds
(without alignments)
1085.275 Million cell updates/sec

Title: US-09-778-961-2

Perfect score: 2518

Sequence: 1 MRELVGSGRYDTQDFSVL.....RCRRGGRREDPPMSLRTVAL 472

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2492	99.0	1458	13	US-10-054-691-2
2	2492	99.0	1458	16	US-10-478-245-1
3	2407	95.6	1423	15	US-10-092-900A-86
4	2336.5	92.8	1419	15	US-10-092-900A-82
5	1185	47.1	267	15	US-10-276-774-1423
6	1185	47.1	267	15	US-10-296-115-1339
7	894.5	35.1	969	16	US-10-478-245-9
8	599.5	23.8	382	15	US-10-369-493-7025
9	551.5	21.9	414	15	US-10-369-493-5575
10	527	20.9	101	15	US-10-264-237-1728
11	527	20.9	148	10	US-09-764-891-4078
12	465.5	18.5	270	15	US-10-094-749-2029
13	456.5	18.1	310	15	US-10-092-900A-84

14	414	16.4	981	15	US-10-369-493-5416	Sequence 5416, Ap
15	406.5	16.1	348	15	US-10-369-493-6523	Sequence 6523, Ap
16	336.5	13.4	349	15	US-10-369-493-6522	Sequence 6522, Ap
17	329	13.1	425	15	US-10-369-493-5161	Sequence 5161, Ap
18	233.5	9.3	132	15	US-10-276-774-1607	Sequence 1607, Ap
19	136	5.4	300	14	US-10-156-761-13312	Sequence 13312, A
20	106	4.2	690	16	US-10-437-963-178287	Sequence 178287, A
21	102.5	4.1	462	15	US-10-120-835-36	Sequence 36, Appl
22	102.5	4.1	462	15	US-10-120-835-40	Sequence 40, Appl
23	102	4.1	773	16	US-10-437-963-178758	Sequence 178758, A
24	102	4.1	1063	16	US-10-437-963-157323	Sequence 157323, A
25	99.5	4.0	1027	16	US-10-408-765A-1609	Sequence 1609, Ap
26	99.5	4.0	1028	14	US-10-153-668-192	Sequence 192, App
27	99	3.9	646	15	US-10-335-977-5174	Sequence 5174, Ap
28	99	3.9	810	9	US-09-815-242-5586	Sequence 5586, Ap
29	99	3.9	818	9	US-09-815-242-12424	Sequence 12424, A
30	99	3.9	818	9	US-09-815-242-12789	Sequence 12789, A
31	99	3.9	818	15	US-10-282-122A-44278	Sequence 44278, A
32	98.5	3.9	426	15	US-10-335-977-8573	Sequence 8573, Ap
33	98.5	3.9	458	15	US-10-422-536-3	Sequence 3, Appli
34	98.5	3.9	839	16	US-10-468-250A-66	Sequence 66, Appl
35	98.5	3.9	1004	16	US-10-473-276-3	Sequence 3, Appli
36	98.5	3.9	1010	15	US-10-441-147-18	Sequence 18, Appl
37	98.5	3.9	1460	14	US-10-128-714-8301	Sequence 8301, Ap
38	97.5	3.9	524	15	US-10-335-977-8574	Sequence 8574, Ap
39	97.5	3.9	633	14	US-10-168-843A-28	Sequence 28, Appl
40	97.5	3.9	640	8	US-08-834-666A-14	Sequence 14, Appl
41	97.5	3.9	641	15	US-10-282-122A-58899	Sequence 58899, A
42	97.5	3.9	791	15	US-10-104-047-3286	Sequence 3286, Ap
43	97	3.9	417	16	US-10-437-963-145671	Sequence 145671, A
44	96.5	3.8	472	15	US-10-425-114-47664	Sequence 47664, A
45	96.5	3.8	3662	16	US-10-437-963-166059	Sequence 166059, A

ALIGNMENTS

RESULT 1

US-10-054-691-2
; Sequence 2, Application US/10054691
; Publication No. US20020115846A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020115846A1el Human Lipase and Polynucleotides Encoding t
; FILE REFERENCE: LEX-0303-USA
; CURRENT APPLICATION NUMBER: US/10/054,691
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 60/264,049
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1458
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-054-691-2

Query Match 99.0%; Score 2492; DB 13; Length 1458;
Best Local Similarity 93.7%; Pred. No. 1.2e-226;
Matches 472; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Qy	1	MRELVGSGRYDTQDFSVLQPPFQNTQLPVL-----	33
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Qy	34	-----LEPLGSKETLDRAMPITCTQNEPFLTRPNSNYTPIKPAINWGSDFLCT	88
Db	1015	LWTNMLEPLGSKETLDRAMPITCTQNEPFLTRPNSNYTPIKPAINWGSDFLCT	1074
Qy	89	EWKASNSVPTSVHOLRPADIKVVAALGDSLTAVGARNSSDLPTSWRGLSWISGDN	148

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OTHER INFORMATION: Incyte ID No: 2440624CD1
US-10-478-245-1
Query Match 99.0%; Score 2492; DB 16; Length 1458;
Best Local Similarity 93.7%; Pred. No. 1.2e-226;
Matches 472; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MRELVGSRDYTDQDFSVVLQPPFQNTQLOLVLA----- 33
DB 955 MRELVGSRDYTDQDFSVVLQPPFQNTQLOLVLA----- 1014
QY 34 -----LPLGSGKTTDLRAEMPITCTQNEPFLRTPRNSNYTYPIKPAIENWGSDFLCT 88
DB 1015 LWTNMLEPLGSKTTDLRAEMPITCTQNEPFLRTPRNSNYTYPIKPAIENWGSDFLCT 1074
QY 89 EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARNSSDLPTSWRGLSWSIGDGN 148
DB 1075 EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARNSSDLPTSWRGLSWSIGDGN 1134
QY 149 LETHHTLNLKKNPYLLGFSTSTWGTAGLNVAAGARADMPAQAWDLVERMKNSPD 208
DB 1135 LETHHTLNLKKNPYLLGFSTSTWGTAGLNVAAGARADMPAQAWDLVERMKNSPD 1194
QY 209 INLEKDWKLVTLFIGVNDLCHYCENPEAHATEYVQHIQQALDILSEELPRAFNVEVM 268
DB 1195 INLEKDWKLVTLFIGVNDLCHYCENPEAHATEYVQHIQQALDILSEELPRAFNVEVM 1254
QY 269 ELASLYQGGKCAMLAANNCTCLRHSSOSLEKQELKKNVNNLQHGSSFSYWHQYTOR 328
DB 1255 ELASLYQGGKCAMLAANNCTCLRHSSOSLEKQELKKNVNNLQHGSSFSYWHQYTOR 1314
QY 329 EDFAVVQPPFQNTLTPLNERGDTDLTFSEDCPFHSDRGHAEMAIALWNNMLEPVGRT 388
DB 1315 EDFAVVQPPFQNTLTPLNERGDTDLTFSEDCPFHSDRGHAEMAIALWNNMLEPVGRT 1374
QY 389 TSNNFTHSRKCLKCPSPESPYLYTLRNSRLLPQAEAPVLYWAVPVAAGVGLVVGIIIG 448
DB 1375 TSNNFTHSRKCLKCPSPESPYLYTLRNSRLLPQAEAPVLYWAVPVAAGVGLVVGIIIG 1434
QY 449 TVWRCRRGRRRPPMSLRTVAL 472
DB 1435 TVWRCRRGRRRPPMSLRTVAL 1458

RESULT 3
US-10-092-900A-86
; Sequence 86, Application US/10092900A
; Publication No. US20040043392A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Saha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha T.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.

US-10-478-245-1
; Sequence 1, Application US/10478245
; Publication No. US20040171009A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;
; APPLICANT: YUE, Henry; AZIMZAI, Yalda;
; APPLICANT: BAUGHN, Mariah R.; BUREFORD, Neil;
; APPLICANT: REDDI, Roopa; CHAWLA, Narinder K.;
; APPLICANT: DAS, Debopriya; NGUYEN, Daniel S.;
; APPLICANT: YAO, Monique G.; ARVIZU, Chandra S.;
; APPLICANT: LU, Yan; GANDHI, Ameena R.;
; APPLICANT: GRIFFIN, Jennifer A.; ELLIOTT, Vicki S.;
; APPLICANT: RAMKUMAR, Javalaxmi; LAL, Preeti G.;
; APPLICANT: LU, Dyung Aina M.; LEE, Ernestine A.;
; APPLICANT: LEE, Soo Y.; YUE, Huibin;
; APPLICANT: YANG, Junming; TRIBOULEY, Catherine M.;
; APPLICANT: KABLE, Amy E.; SWARNAKAR, Anita
; TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES
; FILE REFERENCE: PI-0427 USN
; CURRENT APPLICATION NUMBER: US/10/478,245
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/15688
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/292,242
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/293,726
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/295,346
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/303,404
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 60/314,754
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/351,262
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/368,799
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 1458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

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Db      1339  TTNNFTTHSRALKCPSPSPYLYTNRNRLLPDQABEAPVLYWAVPVAAGVGLVVGII 1398
QY      448  GTVWRCRGGRREDPPMSLRITVAL 472
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Db      1399  GTVWRCRGGRREDPPMSLRITVAL 1423
          |||||

RESULT 4
US-10-092-900A-82
; Sequence 82, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Shresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev,, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USSN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USSN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USSN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USSN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USSN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USSN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USSN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 82
; LENGTH: 1419
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-092-900A-82	
Query Match	92.8%; Score 2336.5; DB 15; Length 1419;
Best Local Similarity	89.1%; Pred. No. 6.9e-212;
Matches 450; Conservative	8; Mismatches 8; Indels 39; Gaps 5;
US-10-092-900A-82	
QY	1 MRELVSGRYDQEDSVVLQPFQNIQLPVL-----32
DB	921 MRELVSGRYDQEDSVVLQPFQNIQLPVLQDGLPDTSPFAPDCIHPNKFHSQIARA 980
QY	33 ----ALEPLGSKTETDLRAEMPICTQNEPFLRTPRNSNTYPIKPAIENWGSDFLCT 88
DB	981 LWTNMLEPLGSKTETDLRAEMPICTQNEPFLRTPRNSNTYPIKPAIENWGSDFLCT 1040
QY	89 EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSDLPTSWRGLSWSIGGDN 148
DB	1041 EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSDLPTSWRGLSWSIGGDN 1100
QY	149 LETHHTLPNLIKKNFNYLLGFSSTWGTAGLNVAAGARA-RDMPAQAWDLVERMKNSP 207
DB	1101 LETHHTLPNLIKKNFNYLLGFSSTWGTAGLNVAAGARA-RDMPAQAWDLVERMKNSP 1160
QY	208 DINLEKDWKLVTLFIGVNDLCHYCENPEAHATEYVOHIQOALDILSEELPRAFVNVVEV 267
DB	1161 -IHQEDWKIITLFIGGNDLDFCND----LVGEYVOHIQOALDILSEELPRAFVNVVEV 1215
QY	268 MELASLYOGGKGCAMLAQNNCTCLRHSSOSLSLEKQELKKNVNNLQHGISSFSYWHQYTO 327
DB	1216 MELASLYOGGKGCAMLAQNNCTCLRHSSOSLSLEKQELKKNVNNLQHGISSFSYWHQYTO 1275
QY	328 REDFAVVVQPPFQNTLPLNREGDTLTFPSSEDCFHFSRCHMAEMALANNMLEPVGRK 387
DB	1276 REDFAVVVQPPFQNTLPLN-RGDTDLTFPSSEDCFHFSRCHMAEMALANNMLEPVGRK 1334
QY	389 TTSNFTSHRAKLCPSPEPVLYTLRNSRLLPQAEAPVLYWVPVAAAGVGLVVGII 447
DB	1335 TTSNFTSHRAKLCPSPEPVLYTLRNSRLLPQAEAPVLYWVPVAAAGVGLVVGII 1394
QY	448 GTVWRCRGRGRRPMSRLTRVAL 472
DB	1395 GTVWRCRGRGRRPMSRLTRVAL 1419
RESULT 5	
US-10-276-774-1423	
; Sequence 1423, Application US/10276774	
; Publication No. US20040053245A1	
; GENERAL INFORMATION:	
; APPLICANT: Hyseq, Inc.	
; APPLICANT: Tang, Y, Tom et al	
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides	
; FILE REFERENCES: 21272-030	
; CURRENT APPLICATION NUMBER: US/10/276,774	
; CURRENT FILING DATE: 2002-11-18	
; PRIOR APPLICATION NUMBER: 09/560,875	
; PRIOR FILING DATE: 2000-04-27	
; PRIOR APPLICATION NUMBER: 09/496,914	
; PRIOR FILING DATE: 2000-02-03	
; NUMBER OF SEQ ID NOS: 2700	
; SOFTWARE: Custom	
; SEQ ID NO 1423	
; LENGTH: 267	
; TYPE: PRI	
; ORGANISM: Homo sapiens	
US-10-276-774-1423	
Query Match	47.1%; Score 1185; DB 15; Length 267;
Best Local Similarity	92.3%; Pred. No. 1.2e-103;
Matches 228; Conservative	4; Mismatches 9; Indels 6; Gaps 3;
US-10-276-774-1423	
QY	15 DP---SVVLQPFQNIQLPVL---LALPLGSKTETDLRAEMPICTQNEPFLRTPRNS 68
DB	21 DFLNPTIMRQVFLGNPDKCPVQQAMLEPLGSKTETDLRAEMPICTQNEPFLRTPRNS 80
QY	69 NYTYPIKPAIENWGSDFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPN 128
DB	81 NYTYPIKPAIENWGSDFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPN 140
QY	129 SSDLPTSWRGLSWSIGGDNLETHHTLPNLIKKNFNYLLGFSSTWGTAGLNVAAGARA 188
DB	141 SSDLPTSWRGLSWSIGGDNLETHHTLPNLIKKNFNYLLGFSSTWGTAGLNVAAGARA 200
QY	189 ARDMPAQAWDLVERMKNSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHATEYVOHIQO 248
DB	201 ARDMPAQAWDLVERMKNSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHATEYVOHIQO 260
QY	249 ALDILSE 255
DB	261 ALDILSE 267
Query Match	
Best Local Similarity	
Matches 228; Conservative	
US-10-296-115-1339	
; Sequence 1339, Application US/10296115	
; Publication No. US20040053248A1	
; GENERAL INFORMATION:	
; APPLICANT: Hyseq Inc	
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides	
; FILE REFERENCES: 784PCT	
; CURRENT APPLICATION NUMBER: US/10/296,115	
; CURRENT FILING DATE: 2002-11-18	
; PRIOR APPLICATION NUMBER: US09/488,725	
; PRIOR FILING DATE: 2000-01-21	
; PRIOR APPLICATION NUMBER: US09/552,317	
; PRIOR FILING DATE: 2000-04-25	
; NUMBER OF SEQ ID NOS: 1478	
; SEQ ID NO 1339	
; LENGTH: 267	
; TYPE: PRI	
; ORGANISM: Homo sapiens	
US-10-296-115-1339	
Query Match	47.1%; Score 1185; DB 15; Length 267;
Best Local Similarity	92.3%; Pred. No. 1.2e-103;
Matches 228; Conservative	4; Mismatches 9; Indels 6; Gaps 3;
US-10-296-115-1339	
QY	15 DP---SVVLQPFQNIQLPVL---LALPLGSKTETDLRAEMPICTQNEPFLRTPRNS 68
DB	21 DFLNPTIMRQVFLGNPDKCPVQQAMLEPLGSKTETDLRAEMPICTQNEPFLRTPRNS 80
QY	69 NYTYPIKPAIENWGSDFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPN 128
DB	81 NYTYPIKPAIENWGSDFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPN 140
QY	129 SSDLPTSWRGLSWSIGGDNLETHHTLPNLIKKNFNYLLGFSSTWGTAGLNVAAGARA 188
DB	141 SSDLPTSWRGLSWSIGGDNLETHHTLPNLIKKNFNYLLGFSSTWGTAGLNVAAGARA 200
QY	189 ARDMPAQAWDLVERMKNSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHATEYVOHIQO 248
DB	201 ARDMPAQAWDLVERMKNSPDINLEKDWKLVTLFIGVNDLCHYCENPEAHATEYVOHIQO 260
QY	249 ALDILSE 255
DB	261 ALDILSE 267
Query Match	
Best Local Similarity	
Matches 228; Conservative	
US-10-478-245-9	
; Sequence 9, Application US/10478245	
; Publication No. US20040171009A1	
; GENERAL INFORMATION:	
; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;	
; APPLICANT: YUE, Henry; AZIMZAI, Yalda;	
; APPLICANT: BAUGHN, Mariah R.; BURFORD, Neil;	
; APPLICANT: REDDY, Roopa; CHAWLA, Narinder K.;	

us-09-778-961-2.rapb

Mon Mar 28 09:43:26 2005

61 WAPVAAAGVGLVIGIICITVWVRCRGGRREDPPMSLRTGAL 101

Db
 RESULT 11
 US-09-764-891-4078
 ; Sequence 4078, Application US/09764891
 ; Publication No. US20030077808A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC006
 ; CURRENT APPLICATION NUMBER: US/09/764,891
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 10231
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4078
 ; LENGTH: 148
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-764-891-4078
 Query Match 20.9%; Score 527; DB 10; Length 148;
 Best Local Similarity 78.3%; Pred. No. 1,4e-41;
 Matches 108; Conservative 9; Mismatches 17; Indels 4; Gaps 3;
 QY 34 LEPLGSKTETDLRAEMPITCTONEPFLTRPNNSYTPKPAIENWGSDFLCTEWKAS 93
 Db 11 LEPLGSKTETDLRAEMPITCTONEPFLTRPNNSYTPKPAIENWGSDFLCTEWKAS 70
 QY 94 NSVPTSHQRPADIKVVAALGDSLTAVGARNNSDLPSTWRG-LSWSIGDGNL-ET 151
 Db 71 NSVPTSHQRPADIKVVAALGDSLTAVGARNNSDLPSTWRG-LSWSIGDGNL-ET 130
 QY 152 HTTLPNI--LKKFNPYLL 167
 Db 131 HHTAQHSEEVQPLPWL 148

RESULT 12
 US-10-094-749-2029
 ; Sequence 2029, Application US/10094749
 ; Publication No. US20030219741A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ISOGAI, TAKAO
 ; APPLICANT: SUGIYAMA, TOMOYASU
 ; APPLICANT: OTSUKI, TETSUO
 ; APPLICANT: WAKAMATSU, AI
 ; APPLICANT: SATO, HIROYUKI
 ; APPLICANT: ISHII, SHIZUKO
 ; APPLICANT: YAMAMOTO, JUN-ICHI
 ; APPLICANT: ISONO, YUUKO
 ; APPLICANT: HIO, YURI
 ; APPLICANT: OTSUKA, KAORU
 ; APPLICANT: NAGAI, KEIICHI
 ; APPLICANT: TRIE, RYOTARO
 ; APPLICANT: TAMECHIKI, ICHIRO
 ; APPLICANT: SEKI, NAOHICO
 ; APPLICANT: YOSHIKAWA, TSUTOMU
 ; APPLICANT: OTSUKA, MOTOKYUKI
 ; APPLICANT: NAGAHARI, KENJI
 ; APPLICANT: MASUHO, YASUHIKO
 ; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
 ; FILE REFERENCE: 084335/0160
 ; CURRENT APPLICATION NUMBER: US/10/094,749
 ; CURRENT FILING DATE: 2002-03-12
 ; PRIOR APPLICATION NUMBER: 60/350,435
 ; PRIOR FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: JP 2001-328381
 ; PRIOR FILING DATE: 2001-09-14
 ; NUMBER OF SEQ ID NOS: 3381
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2029

; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 5575
 ; LENGTH: 414
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 ; US-10-369-493-5575
 Query Match 21.9%; Score 551.5; DB 15; Length 414;
 Best Local Similarity 34.4%; Pred. No. 3.3e-43;
 Matches 132; Conservative 56; Mismatches 143; Indels 53; Gaps 10;
 QY 80 NWGSDFLCTEWKASNVPTSHQRPADIKVVAALGDSLTAVGARNNSDLPSTWR 137
 Db 24 NWGSD--ASVMAKSKKVPSTSAHSVRPADIKVIGALGDSLTAVGARNNSDLP 81
 QY 138 GLWSIGDGNLTHHTLNLKKNPILLGF-----STSWEGTAGLNVAAGARADM 192
 Db 82 GLAQIGGDKSLDEHITVANLRFKNPTLVGASKGIGSENWVE-VSHLNMGVGAESKI 140
 QY 193 PAQAWDLVERMKNSPDINLEKWKLVTLFVNDLCHYCENP-----EALHATEYVHQI 247
 Db 141 IGQARALVNTMHAHSEINVKDKLVNIFGANDICVCEDFYFNSTALHGNATEKNI 200
 QY 248 QALDILSEELP-----RAFNVVVEWELASLYQ 275
 Db 201 AAVQLQDNLPRTNFKFKLFSRISVCKTFSWREFKNSIYRTIVSLTGMFNRMLRK 260
 QY 276 GQGGK--CAMLAQNNCTCLRHSSOLEKELKYNWNLQHGISSFSYWHQVTOREDFAV 333
 Db 261 IDKKYFCEGLHT-FECDC--ESNKQFTDDIQGVCFGYNAEKDQNTGLFDNKDDFTF 317
 QY 334 VVQPFQNTL-TPLNERGDTLTFSEDCFHFSRDRGHAEMAIALWNNMLPEVGRKTTSN 392
 Db 318 VVQPFNGILDPVAPSGVVDMTFFADCFHFSAYGHGNIEMHNLWNTIVQVGFQKTSYN 377
 QY 393 FTHSRRAKLKCPSPESPSPSYLYTLRNS 416
 Db 378 LSDPSVGLHCPSTNCPFFPTTKNS 401
 RESULT 10
 US-10-264-237-1728
 ; Sequence 1728, Application US/10264237
 ; Publication No. US20040009491A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birse et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: P431P1
 ; CURRENT APPLICATION NUMBER: US/10/264,237
 ; CURRENT FILING DATE: 2002-10-04
 ; PRIOR APPLICATION NUMBER: PCT/US01/16450
 ; PRIOR FILING DATE: 2001-05-18
 ; PRIOR APPLICATION NUMBER: US 60/205,515
 ; PRIOR FILING DATE: 2000-05-19
 ; NUMBER OF SEQ ID NOS: 2876
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO 1728
 ; LENGTH: 101
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-264-237-1728
 Query Match 20.9%; Score 527; DB 15; Length 101;
 Best Local Similarity 99.0%; Pred. No. 7.8e-42;
 Matches 100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 372 MAIALWNNMLPEVGRKTTSNFTHSRRAKLKCPSPESPSPSYLYTLRNSILLPQAEAEVLY 431
 Db 1 MAIALWNNMLPEVGRKTTSNFTHSRRAKLKCPSPESPSPSYLYTLRNSILLPQAEAEVLY 60
 QY 432 WAPVAAAGVGLVIGIICITVWVRCRGGRREDPPMSLRTVAL 472


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; LENGTH: 270
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2029

Query Match
  18.5%; Score 465.5; DB 15; Length 270;
Best Local Similarity 35.9%; Pred. No. 2.5e-35;
Matches 108; Conservative 39; Mismatches 101; Indels 23; Gaps 7;

Qy 203 MKNSPDINLEKDWKLVTFIGVNDLCHYCNPEAHATEYVQHIOQALDILSELPRAFV 262
Db 1 MKNDTRHFQEDWKIITLFIGGNDLDFCNLDVHYSQNFDTNIGKALDILHAEVPRAFV 60

Qy 263 NVVEVME---LASLYQGQGGKAMLAANNCTC-LRHSQSSLEKQELKKNVNNI-QHGISS 318
Db 61 NLVTVLIVNRLRYQEKVKYCPRMILRSICPCVLKFDNDSTELATLIEFNKKFQETHQ 120

Qy 319 PSYWHQYTOREDFAVVQVQPFONTLTPLNBERGDTDLTFESEDCHPFSDRGHAEMAIALWN 378
Db 121 LIESGRYDTREDFTVVVQPFENVDMPTSEGLPDNSFFAPDCPHFSKSHSRAASALWN 180

Qy 379 NMLEPVGRKTTNNFTHSRALKKCPSPESPLYTLRNS-----RLLPDQAEAEPEVLY-- 431
Db 181 NMLEPVGQKTRHKF-ENKINITCPNQVQFLRTYKNSMQHGTWLPFCR-DRAPSALHPT 238

Qy 432 -----WAVPAAGVGLVVGIIIG-TVVW 452
Db 239 SVHALRPADIQVVAALGDSLTVRTLGPQVWV 269

RESULT 13
US-10-092-900A-84
; Sequence 84, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zernhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Beha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Carterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USSN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/283,675
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; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USSN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USSN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USSN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USSN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USSN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USSN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 84
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-900A-84

Query Match 18.1%; Score 456.5; DB 15; Length 310;
Best Local Similarity 41.6%; Pred. No. 2.2e-34;
Matches 99; Conservative 38; Mismatches 90; Indels 11; Gaps 5;

Qy 203 MKNSPDINLEKDWKLVTFIGVNDLCHYCNPEAHATEYVQHIOQALDILSELPRAFV 262
Db 1 MKNDTRHFQEDWKIITLFIGGNDLDFCNLDVHYSQNFDTNIGKALDILHAEVPRAFV 60

Qy 263 NVVEVME---LASLYQGQGGKAMLAANNCTC-LRHSQSSLEKQELKKNVNNI-QHGISS 318
Db 61 NLVTVLIVNRLRYQEKVKYCPRMILRSICPCVLKFDNDSTELATLIEFNKKFQETHQ 120

Qy 319 PSYWHQYTOREDFAVVQVQPFONTLTPLNBERGDTDLTFESEDCHPFSDRGHAEMAIALWN 378
Db 121 LIESGRYDTREDFTVVVQPFENVDMPTSEGLPDNSFFAPDCPHFSKSHSRAASALWN 180

Qy 379 NMLEPVGRKTTNNFTHSRALKKCPSPESPLYTLRNS-----RLLPDQAEAEPEVLY 431
Db 181 NMLEPVGQKTRHKF-ENKINITCPNQVQFLRTYKNSMQHGTWLPFCR-DRAPSALH 236

RESULT 14
US-10-369-493-5416
; Sequence 5416, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5416
; LENGTH: 981
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5416

Query Match 16.4%; Score 414; DB 15; Length 981;
Best Local Similarity 29.8%; Pred. No. 1.4e-29;
Matches 106; Conservative 63; Mismatches 175; Indels 12; Gaps 7;
```

us-09-778-961-2.rapb

Mon Mar 28 09:43:26 2005

Qy 356 FFEEDCFHSDRGHAEVAIAIAIANNMLEPVGRKTTNNFTHSRAKLKCPSPESPYLYLRN 415
Db 286 FYASDLPHLSKFGHVLAKHYWLNLFEPVGEKTKRADLGDTKPKIYELNEKNCIKTVGN 345
Qy 416 SRL 418
Db 346 SKM 348

Search completed: March 25, 2005, 14:49:39
Job time : 152 secs

84 DFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTAVAGRPNNSSDLPTSWRGLSWSI 143
53 NFNCQPHRKSS--ESVHQLHPSQIGVIAALGDSVSAQAASSSILDLDQPPGVSVFT 110
144 GGDGNLETHHTLPLNFKFNPVLLGFSTSTWEGTAGLNVAAGARMPAQAWDLVERM 203
111 GDDVKLNEQATFINIFRKFAPIKGGSSDFVQKFDYDFNNAIPGFSSELPEQALKASTL 170
204 KNSPDINLEKDWKLVTLFTGVNDLCHYCENPEAHILATEYVQHIQOALDILSEELPRAFN 263
171 KKLGRSDTWFVNFIFIGHNDLNCINNETTFGPETFGKSLHSALTIIQTNPVKVFVN 230
264 VVEVMELASLYQOGG-GKCAMLAQNNCTCLRHSSSLEKQELKK-VNWNLOHGIGSFSY 321
231 IMPPINVKIHSQAHLKSKCFESHRTKSCI-FELNEKEYQNIKKQFDEQLNEVVEQFN- 288
322 WHQYTOREDFAVVVQPPFFQNTLPLNERGDTDLTFSEDCFHSDRGHAEVAIAIAIANNM 381
289 -QKYGNSSTFAVVIAPAMDLSIPL-LKNQPNIGLLALDCPHLSPIAHDIAAKQIWKGLF 346
382 EPVGRKTTNNFTHSRAKLKCPSPESPYLYTLNSRLLPDQAEAPVLYWAVPVA 437
347 EPIDOKTITNQLSVGDFRVCPPVECPYLRTIONS-----ENCEPSREMFRLRVPSA 398

RESULT 15
US-10-369-493-6523
; Sequence 6523, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6523
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6523

Query Match 16.1%; Score 406.5; DB 15; Length 348;
Best Local Similarity 32.2%; Pred. No. 1.5e-29;
Matches 117; Conservative 66; Mismatches 133; Indels 47; Gaps 11;
Qy 74 IKPAIENWGSDFLCTEWKASNSV-----PTSVHQLRPADIKVVAALGDSLTAVAGRPN 127
15 VKMALE-----KYLNISIDPREIYDDVNMKPHHVRVIGAMGDSLT--IGSRAE 61
128 NSSDLPTSWRGLSWSIGDGNLTHHTLPLNLIK-----KFPYLLGFSTSTWEG-TAGLNV 182
62 NIVQQRQRYPGNAPFTGMDPEVDRLHTVYNIPIIAEKTGNKLFGGSGIDYGENYGLNV 121
183 AAEGARADMPAQAWDLVERMKSPDINLEKDWKLVTLFTGVND---LCHYCENPEAHILA 239
122 AIGMKSDDLRQAKELVSRKANKELINENDMKVSLWIGTNDVGTGLVRLDPIP--V 179
240 TEYVQHIQOALDILSEELPRAFNVVEVMELASLYQOGGKCAMLAQNNCTCLRHSSQSS 299
180 DEYKSHIEKGLLYLKENLPRTVISVIGMFFPAQLLQEAQ-----SILKNGKRA 226
300 LEKQELKKNVNLQHGISFSFYHQYTOR---EDFAVVQVQFF-FQNTLPLNERGDTDLT 355
227 RTVENOKKLD-DLSDGYRNVSIDFQNEHFNSNDFTVVQVQFATEYTDTSYRDEHGKYNPT 285

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1933.5	76.8		1458	2	A45665	adult-specific bru
2	599.5	23.8		382	2	T20655	hypothetical prote
3	551.5	21.9		414	2	T26083	hypothetical prote
4	414	16.4		981	2	T16060	hypothetical prote
5	406.5	16.1		348	2	T24016	hypothetical prote
6	336.5	13.4		349	2	T24015	hypothetical prote
7	329	13.1		425	2	T21835	hypothetical prote
8	107	4.2		3655	2	T38084	TRAP-like protein
9	101	4.0		3972	2	S75251	hypothetical prote
10	99.5	4.0		480	2	JC7672	catalase (EC 1.11.
11	99.5	4.0		749	2	C87618	excinuclease ABC,
12	99	3.9		818	2	F89819	endopeptidase [imp
13	99	3.9		913	2	T15278	hypothetical prote
14	99	3.9		1804	2	T34518	neatin - golden ha
15	98.5	3.9		863	2	A55173	cf-9 protein precu
16	98.5	3.9		1010	2	T09499	ATP-dependent clip
17	97.5	3.9		524	2	E71881	hypothetical prote
18	97.5	3.9		641	2	A64667	outer membrane pro
19	97	3.9		575	1	VCLJHD	env polyprotein pr
20	96	3.8		814	2	AE2051	endopeptidase Clp
21	96	3.8		1498	2	B97355	DNA segregation AT
22	95.5	3.8		1540	2	T45619	hypothetical prote
23	95	3.8		362	2	A24710	pifc protein - Esc
24	95	3.8		390	2	T07246	hypothetical prote
25	95	3.8		583	2	E75529	probable peptide A
26	95	3.8		734	2	S37998	probable serine/th
27	94.5	3.8		571	2	T29643	hypothetical prote
28	94	3.7		708	2	H64631	outer membrane pro
29	94	3.7		1014	2	S32613	HEX2protein - yea

Db 1375 TTSNNFTYGRKTKCSPSPSPYLYTLRNSRLLPDQAEADPTVLYWAVFAAGAGLIGIL 1434
QY 448 GTVVMRCRGRGRRDPPMSLRT 469
Db 1435 AMVAGRMCRPRDPPLSLST 1456

RESULT 2
T26055
hypothetical protein F09C8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26055
R;McMurray, A.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19306
A;Accession: T26055
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-382 <WIL>
A;Cross-references: UNIPROT:O01300; EMBL:Z68132; PIDN:CAA92221.1; GSPDB:GN00028; CESP:FO
A;Experimental source: clone F09C8
C;Genetics:
A;Gene: CESP:F09C8.1
A;Map position: X
A;Introns: 7/1; 71/3; 109/1; 164/3; 192/3; 245/2; 263/3; 303/3; 360/3
C;Superfamily: Caenorhabditis elegans hypothetical protein R07B7.8

Query Match 23.8%; Score 599.5; DB 2; Length 382;
Best Local Similarity 37.5%; Pred. No. 7.4e-40;
Matches 132; Conservative 63; Mismatches 118; Indels 39; Gaps 9;

QY 91 KASNSVPTSVHQLRPADIKVVAALGDSLT-----TAVGARPNNSSDLPTSGRWGLSWS 142
Db 35 KSKKVPVTVNSVRPADIKLIALGDSLTVGGLFSSQAANGAGAEADPVAVVLYQRLGAFQ 94

QY 143 IGGDGNLETHHTLPNLIKKNFYLLGFT-----STWEGTAGLVAAEGARADMPAQAW 197
Db 95 AGGDKTLEHVTPINLIKKNFYLLGFT-----TAVGARPNNSSDLPTSGRWGLSWS 153

QY 198 DLAVERMKNSPD-INLEKQKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQAQDLILSEE 256
Db 154 QLVQLQQLQTEVTVNNKEDKWLNIIFGNDICGCRKVEDSPYNCAQDIKQAVQIIYDN 213

QY 257 LPRAFVNVVVEMLASLYGQGGK--CAMLAQNNCTCLRHSSQSLKQELKKVNNWLOH 314
Db 214 VPRVIVSLTGLHLEMLRQTDGHWFCQRL-HHDECGC--ESNKNFTDADIRQACID--- 267

QY 315 GISSFSYWHQYT-----OREDFAVVVQVFFONTLTPLNERGDTDLTFFSDCFHFS 365
Db 268 -----YNKYEKQIETDGTFFKNDFYVYVQPMFQDTLPPWENGKPTQKFFAPDCFHS 320

QY 366 DRGHAEMALMNNMILEPYGRKTTNNFTHSRAKLCSPSPSPYLYTLNRSR 417
Db 321 QWGHALVSVLYNNILQPVGSKSTSVNSMSVPLQLTACPDACPFRTTPKNSQ 372

RESULT 3
T26083
hypothetical protein W02B12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26083
R;Swinburne, J.; Ainscough, R.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z20149
A;Accession: T26083
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-414 <WIL>
A;Cross-references: UNIPROT:Q23119; EMBL:Z66521; PIDN:CAA91393.1; GSPDB:GN00020; CESP:W0
A;Experimental source: clone W02B12
C;Genetics:

A;Gene: CESP:W02B12.1
A;Map position: 2
A;Introns: 5/1; 61/3; 101/1; 156/3; 212/2; 273/2; 297/3; 332/3; 368/3
C;Superfamily: Caenorhabditis elegans hypothetical protein R07B7.8

Query Match 21.9%; Score 551.5; DB 2; Length 414;
Best Local Similarity 34.4%; Pred. No. 5.5e-36;
Matches 132; Conservative 56; Mismatches 143; Indels 53; Gaps 10;

QY 80 NWGSDFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTTA--VGARPNNSSDLPTSWR 137
Db 24 NWSCD--ASVMAKSKKVPVTSVHQLRPADIKVVAALGDSLTAAANGAGAQGDPLAVILOQR 81

QY 138 GLSWSIGGDNLETHHTLPNLIKKNFYLLGFT-----STWEGTAGLVAAEGARADMP 192
Db 82 GLAPQIGGDKSLDEHITVANVLEKFNPTLVGASKGIGSENWVE-VSHLNMGVPGAESKDI 140

QY 193 PAQAWDLIVERMKNSPDINLEKQKLVTLFIGVNDLCHYCENP-----EAHLATEYVQHIQ 247
Db 141 IGGARALVNTMHAHSEINVKEDKWLNIIFGNDICVYCEDPYFNSTALHGNATPEKNII 200

QY 248 QALDILSEELP-----RAFNVVVEVMEELASLYQ 275
Db 201 AAVQILODNLPRTNFRFKLPFRISVCKTFSSWREFKNSNIYSRTIVSLTGMFMRLRK 260

QY 276 GQCGK--CAMLAQNNCTCLRHSSQSLKQELKKVNNWLOHIGISSFSYWHQYTQREDAV 333
Db 261 IDKKKYFCEGLHT-PECDC--ESNKNQFTDDIQQVCFGYMNAEKDIQNTGLFNDKODFTF 317

QY 334 VQVQFFQNTL-TPLNERGDTDLTFFSDCFHFSDRGHAEMALMNNMILEPYGRKTTNN 392
Db 318 VVQVFFNGILPPVYASPGVDMVDTFFADPCFHSAYGHGNCIGMHLNWTIVQVGFQKQTSVN 377

QY 393 FTHSRAKLCSPSPSPYLYTLNRS 416
Db 378 LSDPSVGLHCHSTNCPRPPTTKNS 401

RESULT 4
T16060
hypothetical protein F13H8.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16060
R;Ding, H.
submitted to the EMBL Data Library, July 1995
A;Description: The sequence of C. elegans cosmid F13H8.
A;Reference number: Z18455
A;Accession: T16060
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-981 <DIN>
A;Cross-references: EMBL:U23139; NID:G722370; PID:G722375; PIDN:AAC46681.1; CESP:F13H8.5
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:F13H8.5
A;Introns: 46/1; 124/1; 201/3; 255/2; 419/1; 452/1; 645/3; 666/3; 692/3; 719/3; 794/3; 8;

Query Match 16.4%; Score 414; DB 2; Length 981;
Best Local Similarity 29.8%; Pred. No. 1.7e-24;
Matches 106; Conservative 63; Mismatches 175; Indels 12; Gaps 7;

QY 84 DFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTAVGARPNNSSDLPTSGRWGLSWSI 143
Db 53 NFNCPPQHRKSS--ESVHQLHPSQIGVIALGDSVSAQAASSSSLDLFDQPGFQSVFT 110

QY 144 GGDGNLETHHTLPNLIKKNFYLLGFTSTWEGTAGLVAAEGARADMPAQAWDLIVERM 203
Db 111 GDDVKLNEQATFINIFKFPAPRIKGGSSDPVQKPYDFNMAIPGSPSELPQALKLASTL 170

QY 204 KNSPDINLEKQKLVTLFIGVNDLCHYCENPEAHLATEYVQHIQQAQDLILSEELPRAFN 263
Db 171 KKKLGRTSDTWKRVNIFIGHNDLCNINNETTFGPGTFCGLSHSALTITIQTVNPKVFN 230

Qy 73 PIKPAIENWGSD--FLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTITAVGARPNNS 129
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 113 PVAGVINSAFNRDKTSCPRINTELLTGTVNGNISPEDITIIAAMGDALLATIGLWPN-- 170

QY 360 -----DCFHSD-----RGHAEMAIAMNNMLPVGKRTTNNFTSHRAKLC 402
DB 1021 KLAANNVIVHDIFYADVIOGNHKTFTNLQKEVI-----ISPHYFAHCLSEVVC 1069

RESULT 9
S75251
hypothetical protein sir1028 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S75251
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.
S:
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S75251
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-3972 <KAN>
A:Cross-references: UNIPROT:P71139; EMBL:D90904; GB:AB001339; NID:G1652225; PIDN:BAAL1716;
C:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: Synechocystis hypothetical protein sir1028

Query Match 4.0%; Score 101; DB 2; Length 3972;
Best Local Similarity 27.3%; Pred. No. 1.1e+02;
Matches 47; Conservative 24; Mismatches 67; Indels 34; Gaps 9;

QY 50 MPITCPTQNEPFLTPRNSNTYPIKPAIENWGSDFLCTE-----WKASNSVPT-- 98
DB 2792 VPINQASNNGPTLVAFNDELIVFVFDASDN---DILYSSSNPGSSGWDGTSTVLTPS 2848

QY 99 SVHQLR--PADIKVVAALGDSLTAVGARN-----NSDLPTSVRGLSWISIGGD 146
DB 2849 DVNQATNPFLSATVPGL--DGTTLAVFRSNNSPATVGLNLSDDV--TNWQGSALQTQVD 2906

QY 147 GNLETHHTLPNLIKFNPIYLLGFSTWEGTAGLVNAEGARADMPAQAWD 198
DB 2907 ANSQVSLTQVD-----GTYYLFTTST--EASASYATSTDGLNWGDITLIPWD 2952

RESULT 10
JC7672
catalase (EC 1.11.1.6) - Desulfovibrio vulgaris
C:Species: Desulfovibrio vulgaris
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: JC7672
R:Kitamura, M.; Nakanishi, T.; Kojima, S.; Kumagai, I.; Inoue, H.
A:Title: Cloning and expression of the catalase gene from the anaerobic bacterium Desulf.
A:Reference number: JC7672; MUID:21125589; PMID:11226874
A:Accession: JC7672
A:Molecule type: DNA
A:Residues: 1-480 <KIT>
A:Cross-references: DDBJ:AB020341
C:Comment: This enzyme, one of the hemoproteins, located in the cytoplasm, functions as
C:Genetics:
A:Gene: kat
C:Superfamily: catalase
C:Keywords: oxidoreductase

Query Match 4.0%; Score 99.5; DB 2; Length 480;
Best Local Similarity 23.7%; Pred. No. 6.2;
Matches 89; Conservative 39; Mismatches 125; Indels 123; Gaps 24;

QY 37 LGSXTETDLRAEMPICTPTQNEPFLTPRNSNTYPIKPAIENWGSDFLCTEWSKASNV 96
DB 125 VGNNTPTVFLRD--PLKFPDLNHAVKRDPRTN-----MRSKXNW--DF-----TSL 168

QY 97 PTVSHLRPADIKVVAALGDSLTAVGARNNSDLPTSVRGLSWISIGGDGNLEHTLTP 156

QY 130 SLDPTSWRGLSWISIGDGNLEHTLTPNLLKFNPNVLLGFSTSTWEGTAG--LNVAAEGA 187
DB 171 ADI--BFRGASFFIGDSTGDTLITIPNLRFSFKVLGVSHGMCADLPNQLNVAVTGA 228

QY 188 RARDMPAQAWDLVERMKNSPDINLEKDKLVTLFIVGNDLCHYCNPRHAHLATEYVQHIQ 247
DB 229 TTDELPOARLRLTKLSELVDYHNEWIMIIITIGTEELCSRCGSPS-----YDNIR 281

QY 248 QALDILSEELPRAPVNVVWELASLYQOGGKCAMLAQNNCTCLRHSSQSLKQELKK 307
DB 282 KATEHLQIEIPKALVLLGPVHVSFHE---QKSNLLKAR--CACSRDQTEGFMVDVSRK 336

QY 308 VNNW-----LQHGSSFSYWHQVTOREDPAVVVQFPFNTLPLNERGDTDLTFFS 358
DB 337 --WSKVWRDQKVFENG-----TAPTEGMISYPMV--TIIRYPSG-----LFI 378

QY 359 EDCFHSDRGHAEMAIAMNNMLPVGKRTTNNFTSHRAKLCPS 404
DB 379 RDKPLNRRGHYATKWMNRLIG--GDLYNLSSATLSODNYFCPS 422

RESULT 8
T38084
TPAP-like protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R:Gentles, S.; Odell, C.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, November 1995
A:Reference number: 221768
A:Accession: T38084
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-3655 <GEN>
A:Cross-references: UNIPROT:Q10064; EMBL:Z68136; PIDN:CAA92239.1; GSPDB:GN00066; SPDB:SH
A:Experimental source: strain 972h; cosmid clp5
C:Genetics:
A:Gene: SPDB:SPAC1F5.11c
A:Map position: 1
A:Introns: 22/1

Query Match 4.2%; Score 107; DB 2; Length 3655;
Best Local Similarity 20.4%; Pred. No. 31;
Matches 97; Conservative 63; Mismatches 169; Indels 146; Gaps 22;

QY 24 FQNIQPLVL--ALEPIGSKTETDLRAEMPI-----TCPTQNEPFLR----- 63
DB 645 FLNILLRFLLSRIEELGSS---DIRHGSVLLRLFLSFVTVSMFATENEPLVPYVSEI 700

QY 64 -----TPRNSNTYPIKPAIENWGSDFLCTEWSKASNVPTSVHQLRPADIKVVA 113
DB 701 IVKCMKLAIPANSANLNYLLRALFRGIGGRFESDIK---EVMPLHALLLEAFNSLL-- 755

QY 114 LGDSLTTAVGARNNSDLPTS-----WRGLSWISIGDGNLET--- 151
DB 756 -----ISARTPEKDLFTELCLTIPVRLSILLPYMSYLMRPLVMSLKSQLVSOGL 807

QY 152 ---HTTLPNLIKXP-----NPYLLGFSTW-----EGTAGLVNAEGARAD 191
DB 808 RTEPLCLDNLTPDPLDIPAPYIEDLMNLWSHLOPLPYNHNSHTALKILKLGRRRK 867

QY 192 MPQAOWDLVERMKNSPDINLEKDKLVTLFIVGNDLCHYCNPRHAHLATEYVQHIQ 249
DB 868 L-----LDRVQSLKSNPFEN--NFTLLLSIKGVKQQLLH-----YTQVDEA 909

QY 250 LDILSEELPRAPVNVVE-----VNELASLYQOGGKCAMLAQNNCTCLRHSSQSLKQ 304
DB 910 VNLLSS--PSSDLEVKQAFTYVCNISKLYVYKSDATNSLARSICRTADKISKSNDFRR 967

QY 305 LKVNWNLOHGSSFSYWHQVTOREDPAVVVQ-----FFONTLTPNERGDTDLTFFSE 359
DB 968 PYSVIPSRMTGRSSFT---QLSDSDTEIILASATYGLFATTVDLELRE-----EAYFWLE 1020

```
Db 169 PRALHQ-----VTVVMSD-----RCIPASRYRHH-----GFGS-----HTFS 200
Qy 157 NILKFNYPYLLGFSTSTWEGTAGLNVA-AEGARADMPAQAWDLVE-----RMKNSP 207
Db 201 FISPQNQRWYKFLHRTQOGIKNLTDAEAAIVARDESHQDLYDSIERGDFPFWNTYV 260
Qy 208 DINLEKD-----W-----KLVTLFGVNDLCHYCENPRAHLATYVQHIOAL 250
Db 261 QVMPEKDAEKLPHYHFDLTQVWFHKDCPLIEGVLEL---NRNPE-----NYFAEVEQA- 311
Qy 251 DILSEELPRAF--VNVVMEELASLYQOG-----GKCAMLAQQNCTCLRH 295
Db 312 -----AFNPANVPGISFSPDKMLQGRLFSGDAHRVRLGVNHHLLIPVNAARCPVH 362
Qy 296 SQSSLEKQELKKNVNNLQHGSSFSY-----WHQYTORDEDFAVVQFPFQNTLTPLNERGD 351
Db 363 ---SVHRDGMARVDGN--HG-STLAYEPNSYGEWQEPDFA---EP-----PLAIRGD 406
Qy 352 TDLTFPSEDCFHFSR 367
Db 407 AAHWNFREDDADYDQ 422

RESULT 11
C87618
excinnuclease ABC, subunit B [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: C87618
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: C87618
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-749 <STO>
A:Cross-references: UNIPROT:Q9A462; GB:AE005673; NID:gl3424613; PIDN:AAK24943.1; GSPDB:C
C:Genetics:
A:Gene: CC2981
C:Superfamily: excinnuclease ABC chain B

Query Match 4.0%; Score 99.5; DB 2; Length 749;
Best Local Similarity 22.8%; Pred. No. 12;
Matches 79; Conservative 50; Mismatches 139; Indels 79; Gaps 17;

Qy 68 SNYTIPIKPAIENMGSDPLCTEWKASNVPTSVH-QLRPADIKVVAALGDSLTAVGARP 126
Db 404 AEYGFRLPSALDNRPLKF--EWDAMR--POSVHVSATPANWELERAGGVFAEQVI--RP 457
Qy 127 NNSDLPSTWGLSWSIGGDNLET-----HTTLPNII-KKNPYLLGFST 171
Db 458 TGLIDPPVPEVPVS-----KQASQVDDVDVBIQTIQGYRTLVTLTQKMAEDLTETLT 513
Qy 172 STWEGTAGLNVAEGARADMPAQAWDLVERMKNSPDINLEKDWKLVTLFGVNDLCHYC 231
Db 514 E-----QGIRVYVHSDV-DTIEIEIIRDLRGH-----FDVLGINLLREGL 556
Qy 232 ENPRAHLATYVQHIQQALDILSBEELPRAFNVNVVMEELASLYQOGGKCAMLAQQNCT 291
Db 557 DIPEGGLVA-----ILDADKEGFLRSETSLIQTIGRAA--RNVDGK-VILYADVRTG 605
Qy 292 CLRHSQSLEKQELKKNVNNLQHGSSFSYWHQYTORDEDFAVVQFPFQNTLTPLNERGD 351
Db 606 SMERAMAEATARRRRKQAYNLEHGITPES-----VGRDIKDILNSPY-----BRGD 651
Qy 352 -----TDLTFPSEDCFHFSR--HARMATALWNNMLEPVR 386
Db 652 RVLVPMGMSETDDRPFGDNFKAALKQLEAKQREAAANLEFETAAR 697
```

```
RESULT 12
F89819
endopeptidase [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: F89819
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ocu
ma, A.; Mitutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: F89819
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-818 <KUR>
A:Cross-references: UNIPROT:Q9W978; GB:BA000018; PID:gl3700415; PIDN:BAB41713.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:
A:Gene: clpC
C:Superfamily: endopeptidase Clp ATP-binding chain

Query Match 3.9%; Score 99; DB 2; Length 818;
Best Local Similarity 21.6%; Pred. No. 15;
Matches 97; Conservative 51; Mismatches 119; Indels 182; Gaps 25;

Qy 106 ADIKVVAALGD---SLTTAVGARPNSSDLPTSWRGLSWSIGGDNLE-----THTTTL 155
Db 134 ARAQVVALGNPENSNNKNAQAKSNNTPTDLSLARDUT-VIAKQGTLDPVIGRDKETRV 192
Qy 156 PNILK---KFNPYLLGFSTWEGTAGLNVAAG-ARA-----RDMPAQAWDL-- 199
Db 193 IEVLSRRTKKNPVLIIG-----EPGVGKTAIEAGLAQAIIVNNEVPETLKDKRVMSLDNGT 246
Qy 200 -----VERMKN-----SPDI-- 209
Db 247 VVAGTKYRGEFEERLKKVMBEIQAGNVILFIDELHTLVAGAGAGDAIDASNILKPALAR 306
Qy 210 -----NLEKDWKL-----VTLFGVNDLCHYCENPEA 236
Db 307 GELOCIGATTIDYRKNIEKDAALERRFPQVQVDEPSVDTVAIKGLRD-----RYEA 360
Qy 237 H-----LATEYVQH---IQQALDILSBEELPRAFY-----NVVVMELA 271
Db 361 HHRINISDEAIEAAVKNLNRVSDRFLPDKAIDLIDRASSKVRKLSHTTPNNLKEIEQ-- 418
Qy 272 SLYQGGGKCAMLAQ--NNCTCLRHSQSLEKQ-ELKKVNW-NLQHGSSFSFWHQYTQ 327
Db 419 EIEKVKNEKDAVHAQEFENAAANLRDKQTKLEQYERAKNEWKNQAQNGMST-----SLS 472
Qy 328 REDPAVVVQFPFQNTLTPLNERGDTDLTFPSEDCFHFSRCHARMATALWNNMLEPVR 387
Db 473 EEDIAVIAWTGIPILTKINE---TE-----SEKLSLEDTLHERV-----IQOK 514
Qy 388 TTNSNFT---HSRAKLKCPSP-PESPPLY 411
Db 515 DAVNSISKAVRRARAGLKDPRKPGISFIP 543

RESULT 13
T15278
hypothetical protein R155.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T15278
R:Giesel, C.; Wamaley, P.; Kramer, J.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid R155.
A:Reference number: Z18321
A:Accession: T15278
A>Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-913 <GEI>
```


A;Cross-references: UNIPROT:O01922; EMBL:AF003390; NID:g2088866; PID:g2088867; PIDN:AABE
A;Experimental source: strain Bristol N2; Clone R155
C;Genetics:
A;Gene: CRSP:R155.4
A;Map position: 3
A;Introns: 47/1; 68/1; 355/1; 719/1; 794/2; 864/1

Query Match 3.9%; Score 99; DB 2; Length 913;
Best Local Similarity 21.1%; Pred. No. 17; Mismatches 202; Indels 160; Gaps 28;
Matches 116; Conservative 72

QY 2 RELVGSRYDYO-EDRSVLQPFQNIQ-----LP-----VLALPGLGSKT 41
DB 375 KEIMRIGSLATKLSQSAIISPLAGKVQDIKIGSLPAESDKNLTFLKALITDMETLTSKF 434
QY 42 ETLDRAMPITCTONEPFLTRPSNYTY-----PIKPALENWGSDFLCTENKASNVPT 98
DB 435 VALN---EM---VKTIND--LKKDNDSDALQRMSTIVGVNNTYDQKLOETKASKDFPV 486
QY 99 SVHQLRPADIKVVAALGDSLTAVGARPNNSSDLPTSWRGLSWSIGDGNLHTHTLPLNI 158
DB 487 I-----NULLNVNNSISFLNSOPTM-----KKTAEISIADA 517
QY 159 LKKNPYPYLLGFSTWGTAGLVAAE-----GARADMPAQAWDLVERMKNSPD 208
DB 518 LK--NPDLVLAITANQIFEVINSINTIPEIKPVISAIAKAPPEATSVPLV---ITSVAKILPD 572
QY 209 INLEKDWKLVTLFGVNDLCHYCNPEAHILATEVQHIQALDILSEELPRAFNVVVVM 268
DB 573 I--KDDMKNLQTFVSKN-----SNKYK-----ESSVIL--KELNA--TVQLS 611
QY 269 ELASLYQGGGKCAMLAQNNCTCLRHSSQSLKEQLKKNVNNLQHGISSFSYWHQYTOR 328
DB 612 VIGSVARGIFRMEQALGLTNDVSNMK-SFEAVVXDEMSKVLD-----GTDK 657
QY 329 EDFAVV-----QFFQNTLPLNERGDTLTFSEDCPHFSDRGHAEMAI-- 374
DB 658 KMKVLLIGLGLDELEKLLSDLLFVKSVPKSNSTNLADPAGIFEAARKVGVPHFMAIKA 717
QY 375 -----ALMNNMLEPVGRKTTNNFTSHRAKLCPSPPSPYL--YTLRN 415
DB 718 SVLKLMEANNSLAGLLPILNN-LESIGLNFSSFSKSKQLKVLDTSPASLNNNTINN 776
QY 416 SRL--PDQAEAPVL--YVAVPVAGVGLVGI---IGTVVRCRGR-----R 460
DB 777 SRLASTNAQEPGALAKHTIYVIGPLLIIVAVGVVWTVWRRRSQRRRAEAPHR 836
QY 461 EDP-PMSLRT 469
DB 837 NDPTPSRRS 846

RESULT 14
T34518 nestin - golden hamster (fragment)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34518
R;Steinert, P.M.; Chou, Y.H.; Prahlad, V.; Parry, D.A.D.; Marekov, L.; Wu, K.C.; Jiang, S
Submitted to the EMBL Data Library, December 1998
A;Description: A high molecular weight intermediate filament associated protein in BHK-2
with type III vimentin and type IV a-internexin.
A;Reference number: 221538
A;Accession: T34518
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1804 <STE>
A;Cross-references: UNIPROT:Q921Q1; EMBL:AF110498; NID:g4063502; PID:g4063503; PIDN:AAC9
A;Experimental source: cell line BHK-21

Query Match 3.9%; Score 99; DB 2; Length 1804;
Best Local Similarity 22.0%; Pred. No. 48; Mismatches 156; Indels 134; Gaps 23;
Matches 97; Conservative 53

QY 29 LPVLALEPLGSK-TEFLDLRAEMPTCTONEPFLTRPSNYTYPIKPALENWGSDFLC 87
DB 156 LPVLSPTPLSPDPDL-----ETPVATFLKQEFLOARIPILASTPIPPMTI---APCLA 208
QY 88 TEWKASNSVPTSVHQLR-----PADIKVVAALGDSLT-----AVGARNNSDLPTS 135
DB 209 KAEVRAQADAPLSLLQTOGERQQAPEPLWAKATASVSTGVLTELEAGGQQFGHPFEDATA 268
QY 136 WRGLSWSIGDGNLHTHTLPLNKKFNPYLLGFSTWGTAGLVAAEGARA-RDWPA 194
DB 269 -----SAPS-LSPHPVL-----EAKDGDSTRSGSSIFQDEG 301
QY 195 QANDLVERMKNSPDINLEKDWKLVTLFGVNDLCHYCNPEAHILATEVYVQHIQ-----QA 249
DB 302 QIWELVEK---EAAIELKVESSLAQ-----ETQEDGLHTEIQQSGPLQKET 346
QY 250 LDILSEELPRAFNVVVVMELASLYQGGGKCAMLAQNNCTCLR---HSQSSL-----E 301
DB 347 LEALGEB-----PLMSLKIQNHETFGK-----ENCNSLRSDVDENQGTILKSPEE 390
QY 302 KOELKK-----VNNLQHGIGSSFSYWHQYTORDFAVVQVPPF--QNTLPLNERGD 351
DB 391 KQTLKLSLEKQVEVETLEKGVPELS---KPLGKEDPRIEDQELMSPEGTLETLSFIGK 447
QY 352 TDLTFSSDCPHFSDRGHAEMAIAMNNMLEPVGRKTTNNFTSHRAKLCPSPPSPYL 411
DB 448 R-----NEEVRSSEENIESLAAFKESQHPJG-----CPEE----- 481
QY 412 TLRNSRLPDQAE-----APE 428
DB 482 IQRVERLIEKEGQESLSPE 501

RESULT 15

CF-9 protein precursor - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 20-Jan-1995 #sequence_revision 20-Jan-1995 #text_change 15-Mar-2004
R;Jones, D.A.; Thomas, C.M.; Hammond-Kosack, K.E.; Balint-Kurti, P.J.; Jones, J.D.G.
Science 266, 789-793, 1994
A;Title: Isolation of the tomato Cf-9 gene for resistance to Cladosporium fulvum by trans
A;Reference number: A55173; MUID:95063912; PMID:7973631
A;Accession: A55173
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-863 <JON>
A;Cross-references: GB:U15936; NID:g563232; PID:g563233
F;717-739/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>

Query Match 3.9%; Score 98.5; DB 2; Length 863;
Best Local Similarity 19.9%; Pred. No. 18; Mismatches 167; Indels 169; Gaps 23;
Matches 98; Conservative 59

QY 44 LDRAMPITCTPTO-----NEPFLTRPSNYTYPIK-----PALENWGSDFLC 87
DB 18 LALSSSLPHLCPEQDQALSLLQFKNNFTINPNASDYDIRTYVDIQSYPTLSMKNKSTSC 77
QY 88 TEWKASNSVPTSVHQLRPADIKVVAALGDSLTAVGARNNSDLPTSWRGLSWSI--- 143
DB 78 CSMWGVHCDETT-GQVIALDLRCSQIQGKPHNSLSFLQSLNKLRLDLSENFNFTGSLISPK 136
QY 144 -GGDGNLHTHTLPLNKKFNPYLLGFSTWGTAGT-----GLNVA 183
DB 137 FGFSNL--TH-----LDLSHSSFTGLIPSLPBIKSLHLVLRICDQYGLSL- 180
QY 184 AEGARADMPAQAWDLVERMKNSPDINLEK-----DWKLVTLFGVNDL----- 227
DB 181 -----VPYNPELLIKNLTLQRLNLESNVTSSTIPNSFSLHTLTLQISGTELHILP 232
QY 228 -----CHYCENP-----AHLATEVYVQHIQQALDILSEELPRAFN 263

Db 233 ERVFLHSLNLSVNPQLTVRPFTTKWNSASLMTLYVDSVN-----IADRIKPSF-- 285

Qy 264 VEVNELASLYQGQGGKCAM-----LAAQNNCTCLRHSQSLEK-----QELKK- 307

Db 286 ----SHLTSLHLYMGRCNLGPIPKPLWNLTNIVFLHLDGNHLEGPISHFTIFEKLR 341

Qy 308 --VANNLQHGISSFSYWHQYTOREDFAVVVQPPQNTILT----PLNERGDTDLTFESEDCE 362

Db 342 SLVANNFDGGLEFLSF-NTQLERLDLS-----SNSLTGPIPSNISGLQNL-----ECL 388

Qy 363 HFSDRGHAEMAIALWNNNMLEPVGRKTTNN-----FTHSRALKKCPSP 406

Db 389 YLSS-NHLNGSIPSWIFSLPSLVELDLSNNTFSGKIQEFKSKTILSAVTLKQNLKGRIPN 447

Qy 407 SPYLYTLRNSKLL 419

Db 448 S--LLNQKNLQLL 458

Search completed: March 25, 2005, 14:37:16
Job time : 51 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 25, 2005, 14:19:02 ; Search time 180 Seconds
(without alignments)
1342.785 Million cell updates/sec

Title: US-09-778-961-2
Perfect score: 2518
Sequence: 1 MRELVGSRVDTQDFSVL.....RCRRGRRPPMSLRTVAL 472

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2270	90.2	423	Q8IUP7	Q8IUP7 homo sapien
2	1933.5	76.8	1458	1 PHLX_RABIT	Q05017 oryctolagus
3	1764	70.1	1463	2 O70320	Q04728 rattus norv
4	1715.5	68.1	1450	2 O54728	Q54728 rattus norv
5	841	33.4	488	2 Q8P1J6	Q8P1J6 homo sapien
6	635	25.2	186	2 Q8K255	Q8K255 mus musculu
7	613.5	24.4	374	2 O01300	O01300 caenorhabdi
8	577.5	22.9	382	2 Q23119	Q23119 caenorhabdi
9	575.5	22.9	348	2 O7Q05J6	O7Q05J6 anopheles g
10	563	22.4	331	2 O7P139	O7P139 anopheles g
11	560	22.2	373	2 O7PCU2	O7PCU2 anopheles g
12	559.5	22.2	398	2 Q8MXQ8	Q8MXQ8 caenorhabdi
13	552	21.9	377	2 Q3N224	Q3N224 caenorhabdi
14	545.5	21.7	330	2 O7Q7K2	O7Q7K2 anopheles g
15	544.5	21.6	330	2 O7Q912	O7Q912 anopheles g
16	521	20.7	424	2 O3VW80	O3VW80 drosophila
17	504	20.0	447	2 O3VW88	O3VW88 drosophila
18	465.5	18.5	270	2 Q6D9P9	Q6D9P9 homo sapien
19	448	17.8	349	2 O7Q7K3	O7Q7K3 anopheles g
20	430	17.1	394	2 Q3D4Y6	Q3D4Y6 mus musculu
21	414	16.4	460	2 Q95QL1	Q95QL1 caenorhabdi
22	406.5	16.1	348	2 Q21799	Q21799 caenorhabdi
23	355	14.1	565	2 Q814J6	Q814J6 caenorhabdi
24	349	13.9	528	2 P90862	P90862 caenorhabdi
25	345.5	13.7	484	2 Q21798	Q21798 caenorhabdi
26	341.5	13.6	257	2 Q7P8P5	Q7P8P5 anopheles g
27	310.5	12.3	471	2 Q9N4P5	Q9N4P5 caenorhabdi
28	215	8.5	433	2 Q965W0	Q965W0 caenorhabdi
29	136	5.4	300	2 Q82BC2	Q82BC2 streptomyce
30	115.5	4.6	280	2 P96043	P96043 streptococc
31	115	4.6	620	2 Q9GLF7	Q9GLF7 trichosorus

32 113 4.5 305 2 Q9RDP5 Q9rdp5 streptomyce
33 112.5 4.5 417 2 Q7P154 Q7p154 chromobacte
34 108 4.3 491 2 Q7TMR0 Q7tmr0 mus musculu
35 108 4.3 1115 2 Q9HD43 Q9hd43 homo sapien
36 107 4.2 932 2 Q8E589 Q8e589 streptococc
37 107 4.2 3655 1 YAMB_SCHPO Q10064 schizosacch
38 106 4.2 463 2 Q654G7 Q654g7 oryza sativ
39 106 4.2 675 2 Q654G8 Q654g8 oryza sativ
40 105.5 4.2 1433 2 Q8L332 Q8l332 aphanizomen
41 105 4.2 250 2 Q65IC3 Q65ic3 bacillus li
42 105 4.2 373 2 Q9LJP1 Q9ljp1 arabidopsis
43 105 4.2 451 2 Q8R0T8 Q8r0t8 mus musculu
44 105 4.2 491 2 Q8BKX3 Q8bkx3 m mus muscu
45 105 4.2 792 2 Q8MT89 Q8mt89 drosophila

ALIGNMENTS

RESULT 1

Q8IUP7
ID Q8IUP7 PRELIMINARY; PRT; 423 AA.
AC Q8IUP7;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE PLB1 protein.
GN Name=PLB1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchéz A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra W.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
EMBL; BC042674; AAH42674.1; -.
DR Genew; HGNC:30041; PLB1.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR InterPro; IPR001087; Lipase_GDSL.
DR Pfam; PF00657; Lipase_GDSL_1.
SQ SEQUENCE 423 AA; 47354 MW; A20A193491BA780C CRC64;

Query Match 90.2%; Score 2270; DB 2; Length 423;

Best Local Similarity 99.8%; Pred. No. 1.8e-168;

Matches 422; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 50 MPITCPTQNEFFLTPRNSNYTPIKPAIENWGSDFLCTEWKASNSVPTSVHQLRPADIK 109

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1 MPITCPTQNEPFLRTPRNSNYTPIKPAIENWGSDFLCTEWKASNSVPTSVHQLRPADIK 60
110 VVAALGDSLTAVGARNPNSSDLPTSWRGLSWISIGDGNLETHLTPNLKKNPYPYLLGF 169
61 VVAALGDSLTAVGARNPNSSDLPTSWRGLSWISIGDGNLETHLTPNLKKNPYPYLLGF 120
170 STSTWECTAGLNVAAGARADMPAQADLVERMKSPDINLEKDKLVTLPFGVNDLCH 229
121 STSTWECTAGLNVAAGARADMPAQADLVERMKSPDINLEKDKLVTLPFGVNDLCH 180
230 YCENPEAHATEYVQHIOQALDILSELPRAFVNVVEMELASLYQGQGGKCAMLAQNN 289
181 YCENPEAHATEYVQHIOQALDILSELPRAFVNVVEMELASLYQGQGGKCAMLAQNN 240
290 CTCLRHSSQSSLEKQELKKNVNNLQHGISSFSYWHQYQTOREDFAVVVQVFPFNTLPLNER 349
241 CTCLRHSSQSSLEKQELKKNVNNLQHGISSFSYWHQYQTOREDFAVVVQVFPFNTLPLNER 300
350 GDTDLTPFSEDCPHFSDRGHAEMAIALWNNMLPEVGRKTTNNFTSHRAKLKCPSPESP 409
301 GDTDLTPFSEDCPHFSDRGHAEMAIALWNNMLPEVGRKTTNNFTSHRAKLKCPSPESP 360
410 LYTLENSRLLPQAEAEPEVLYWAPVVAAGVGLVVGIIIGTVWRCRRGRRDPPMSLRT 469
361 LYTLENSRLLPQAEAEPEVLYWAPVVAAGVGLVVGIIIGTVWRCRRGRRDPPMSLRT 420
470 VAL 472
421 VAL 423

RESULT 2
PHLX_RABBIT STANDARD; PRT; 1458 AA.
ID AC Q05017;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Phospholipase ADRA-B precursor (EC 3.1.1.-).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Intestine; PubMed=8509424;
RX MEDLINE=93286138;
RA Boll W., Schmid-Chanda T., Semenza G., Mantei N.;
RT "Messenger RNAs expressed in intestine of adult but not baby rabbits. Isolation of cognate cDNAs and characterization of a novel brush border protein with esterase and phospholipase activity.";
RL J. Biol. Chem. 268:12901-12911(1993).
CC -!- FUNCTION: Has esterase and phospholipase A/lysophospholipase activity. Can convert phosphatidylcholine to fatty acids and lipids, possibly including long chain retinyl esters.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Brush border.
CC -!- TISSUE SPECIFICITY: Intestine.
CC -!- DEVELOPMENTAL STAGE: Expressed in the intestine of adult but not baby rabbits.
CC -!- SIMILARITY: Belongs to the "GDSL" lipolytic enzyme family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z12841; CAA78303.1; -.
CC F01; A45665; A45665.

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DR InterPro; IPR001087; Lipase_GDSL.
DR InterPro; IPR008265; Lipase_GDSL_AS.
DR Pfam; PF00657; Lipase_GDSL; 3.
DR PROSITE; PS01098; LIPASE_GDSL_SER; 2.
KW Hydrolase; Repeat; Signal; Transmembrane.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 1458 Phospholipase ADRA-B.
FT DOMAIN 20 1415 Extracellular (Potential).
FT TRANSMEM 1416 1439 Potential.
FT DOMAIN 1440 1458 Cytoplasmic (Potential).
FT DOMAIN 39 1403 4 X 308-326 AA approximate repeats.
FT REPEAT 39 347 1.
FT REPEAT 362 707 2.
FT REPEAT 708 1054 3.
FT REPEAT 1064 1403 4.
FT ACT_SITE 400 400 By similarity.
FT ACT_SITE 747 747 By similarity.
FT ACT_SITE 1103 1103 By similarity.
FT SEQUENCE 1458 AA; 161343 MW; 9D1608F47B1062B6 CRC64;

Query Match 76.8%; Score 1933.5; DB 1; Length 1458;
Best Local Similarity 73.3%; Pred. No. 1.7e-141;
Matches 368; Conservative 39; Mismatches 62; Indels 33; Gaps 2;

QY 1 MRELVSGRYDTQEDFSVVLQPPFQNIQLPVL----- 32
DB 955 LRELVSGRYDTREDFSVVLQPPFQNIQLPVLQDGRDTSFFAPDCVHPNQKHSQLSRA 1014
QY 33 -----ALEPLSKTETDLRAEMPTCTONEPFLRTPRNSNYTPIKPAIENWGSDFLCT 88
DB 1015 LWRNMLEPLGKTDALDLTAITLCTONEPFLRTFRNSDYTPSRPAVENWGSDFLCT 1074
QY 89 EWKASNSVPTSVHQLRPADIKVVAALGDSLTAVGARNPNSSDLPTSWRGLSWISIGDGN 148
DB 1075 ANWASRGVPSVHQLRPADIKVVAALGDSLTAVGARNPNSSDLPTSWRGLSWISIGDGA 1134
QY 149 LETHTLNLKKNPYPYLLGFSTSTWECTAGLNVAAGARADMPAQADLVERMKNSPD 208
DB 1135 LETHTLNLKKNPYPYLLGFSTSTWECTAGLNVAAGARADMPAQADLVERMKNSPE 1194
QY 209 INLEKDKLVTLPFGVNDLCHYCNPEAHATEYVQHIOQALDILSELPRAFVNVVEM 268
DB 1195 IDLEKDKLVTLPFGVNDLCHYCNPEAHATEYVQHIOQALDILSELPRAFVNVVEM 1254
QY 269 ELASLYQGQGGKCA-MLAQNNCTCLRHSSQSSLEKQELKKNVNNLQHGISSFSYWHQYQ 327
DB 1255 ELAGLHQDQGGKCATLLAAQSHCTCFKYSQSSVEMQELKKNVNNLQSGLSRLSYSHQYVQ 1314
QY 328 REDFAVVVQVFPFNTLPLNERGDTDLTFPSDCPHFSDRGHAEMAIALWNNMLPEVGRK 387
DB 1315 REDFAVVVQVFPFNTLPLNERGDTDLTFPSDCPHFSDRGHAEMAIALWNNMLPEVGRK 1374
QY 388 TTSNNFTSHRAKLKCPSPSPYLYTLRNSRLLPQAEAEPEVLYWAPVVAAGVGLVVGII 447
DB 1375 TTSNNFTSHRAKLKCPSPSPYLYTLRNSRLLPQAEAEPEVLYWAPVVAAGVGLVVGII 1434
QY 448 GTVWRCRRGRRDPPMSLRT 469
DB 1435 AMVAGRMRCRPREDDPPLSLST 1456

RESULT 3
QY070320 PRELIMINARY; PRT; 1463 AA.
ID QY070320
AC QY070320;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phospholipase B.
GN Name=PLB;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Caviidae; Cavia.

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OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cri.; TISSUE=Intestine;
RX MEDLINE=98256256; PubMed=9593672; DOI=10.1074/jbc.273.22.13407;
RA Delagebeaudet C., Gassama-Diagne A., Naube M., Ragab A., Li R.Y.,
RA Capeviele J., Ferrara P., Fauvel J., Chap H.;
RT "Ectopic epididymal expression of guinea pig intestinal phospholipase
RT B. Possible role in sperm maturation and activation by limited
RT proteolytic digestion.";
RL J. Biol. Chem. 273:13407-13414 (1998).
DR EMBL; AF045454; AAC40129.1; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR001087; Lipase GDSL.
DR InterPro; IPR008265; Lipase GDSL AS.
DR InterPro; IPR005829; Sug transporter.
DR Pfam; PF00657; Lipase GDSL; 3.
DR PROSITE; PS01098; LIPASE GDSL; 2.
DR PROSITE; PS00217; SUGAR TRANSPORT; 2; UNKNOWN 1.
DR SEQUENCE 1463 AA; 162174 MW; 101C4969815F24B1 CRC64;
SQ
Query Match 70.1%; Score 1764; DB 2; Length 1463;
Best Local Similarity 68.9%; Pred. No. 2.8e-128; Indels 38; Gaps 4;
Matches 348; Conservative 41; Mismatches 78;
Ox 1 MRELVGSGRYDQEDFSVVLQPFQNIQLPVL----- 32
Db 954 MRELVGSGRYDQEDFSVVLQPFQNIQLPVL----- 32
Ox 33 ----ALEPLGSKTETDLRAEMPTCTPQNEPFLTRPNNSNYTPYPIKPAIENWGSDFLCT 88
Db 1014 LWNAMLEPVGSKTETDLRAEMPTCTPQNEPFLTRPNNSNYTPYPIKPAIENWGSDFLCT 1073
Ox 89 EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARNNSDLPSTWRGLSWSIGDGN 148
Db 1074 EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARNNSDLPSTWRGLSWSIGDGN 1133
Ox 149 LETHHTLNLKFNPNYLLGFSTWEGTAGLVAAGARADMPAQAWDLVERMKNQSPD 208
Db 1134 LETHHTLNLKFNPNYLLGFSTWEGTAGLVAAGARADMPAQAWDLVERMKNQSPD 1193
Ox 209 INLEKDWKLTFTGVNDLCHYCENPEAHILATEVQHIQOALDILSBEELPRAFNVEV 267
Db 1194 INLEKDWKLTFTGVNDLCHYCENPEAHILATEVQHIQOALDILSBEELPRAFNVEV 1253
Ox 268 MELASLYOGQGGKC-AMLAQNCTCLRHSSOSLSLEKQELKKNVNLQHGSISSFYWHQYT 326
Db 1254 MELASLYOGQGGKC-AMLAQNCTCLRHSSOSLSLEKQELKKNVNLQHGSISSFYWHQYT 1313
Ox 327 QREDFAVVVQPFQNTLPLNERGDTDLTFSEDCFHFSRDRGHAEMALALNNMMLPEVGR 386
Db 1314 QREDFAVVVQPFQNTLPLNERGDTDLTFSEDCFHFSRDRGHAEMALALNNMMLPEVGR 1373
Ox 387 KTTNNFTHSRALKKCPSPESPYLYTLNRSLLPDQAEAEPEVLYWAVPVVAAAG---VGL 442
Db 1374 KTTNNFTHSRALKKCPSPESPYLYTLNRSLLPDQAEAEPEVLYWAVPVVAAAG---VGL 1433
Ox 443 VGLIGTVVRCRGRREDPPMSL 467
Db 1434 VGLIGTVVRCRGRREDPPMSL 1458

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RESULT 4
O54728 PRELIMINARY; PRT; 1450 AA.
ID O54728
AC O54728
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phospholipase B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SD; TISSUE=Small intestine;
RX MEDLINE=981113187; PubMed=9442065; DOI=10.1074/jbc.273.4.2222;
RA Takemori H., Zolotarov F.N., Ting L., Urbain T., Komatsubara T.,
RA Hatano T., Okamoto M., Tojo H.;
RT "Identification of functional domains of rat intestinal phospholipase
RT B/lipase. Its cDNA cloning, expression, and tissue distribution.";
RL J. Biol. Chem. 273:2222-2231 (1998).
DR EMBL; D63648; BAA23813.1; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR001087; Lipase GDSL.
DR InterPro; IPR008265; Lipase GDSL AS.
DR Pfam; PF00657; Lipase GDSL; 3.
DR PROSITE; PS01098; LIPASE GDSL; 2.
DR SEQUENCE 1450 AA; 161088 MW; 4555898C8FD91F45 CRC64;
SQ
Query Match 68.1%; Score 1715.5; DB 2; Length 1450;
Best Local Similarity 66.9%; Pred. No. 1.7e-124;
Matches 327; Conservative 53; Mismatches 76; Indels 33; Gaps 2;
Ox 1 MRELVGSGRYDQEDFSVVLQPFQNIQLPVL----- 32
Db 959 MRELVGSGRYDQEDFSVVLQPFQNIQLPVL----- 1018
Ox 33 ----ALEPLGSKTETDLRAEMPTCTPQNEPFLTRPNNSNYTPYPIKPAIENWGSDFLCT 88
Db 1019 LWNAMLEPVGSKTETDLRAEMPTCTPQNEPFLTRPNNSNYTPYPIKPAIENWGSDFLCT 1078
Ox 89 EWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARNNSDLPSTWRGLSWSIGDGN 148
Db 1079 EQSPSSKVPTSVHQLRPADIKVVAALGDSLTTAVGARNNSDLPSTWRGLSWSIGDGN 1138
Ox 149 LETHHTLNLKFNPNYLLGFSTWEGTAGLVAAGARADMPAQAWDLVERMKNQSPD 208
Db 1139 LETHHTLNLKFNPNYLLGFSTWEGTAGLVAAGARADMPAQAWDLVERMKNQSPD 1198
Ox 209 INLEKDWKLTFTGVNDLCHYCENPEAHILATEVQHIQOALDILSBEELPRAFNVEV 268
Db 1199 INLEKDWKLTFTGVNDLCHYCENPEAHILATEVQHIQOALDILSBEELPRAFNVEV 1258
Ox 269 ELASLYOGQGGKC-AMLAQNCTCLRHSSOSLSLEKQELKKNVNLQHGSISSFYWHQYT 327
Db 1259 ELASLYOGQGGKC-AMLAQNCTCLRHSSOSLSLEKQELKKNVNLQHGSISSFYWHQYT 1318
Ox 328 REDFAVVVQPFQNTLPLNERGDTDLTFSEDCFHFSRDRGHAEMALALNNMMLPEVGR 387
Db 1319 REDFAVVVQPFQNTLPLNERGDTDLTFSEDCFHFSRDRGHAEMALALNNMMLPEVGR 1378
Ox 388 TTSNFTSHSRALKKCPSPESPYLYTLNRSLLPDQAEAEPEVLYWAVPVVAAAGVGLVGL 447
Db 1379 TTSNFTSHSRALKKCPSPESPYLYTLNRSLLPDQAEAEPEVLYWAVPVVAAAGVGLVGL 1438
Ox 448 GTVVVRCRR 456
Db 1439 GTVVVRCRR 1447

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RESULT 5
O6P1J6 PRELIMINARY; PRT; 488 AA.
ID O6P1J6
AC O6P1J6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LOC388937 protein.
GN Name=LOC388937;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065041; AAH5041.1; ~; DB 2; Length 488;
GO; GO:0003824; F: catalytic activity; IEA.
DR InterPro; IPR001087; Lipase GDSL.
DR InterPro; IPR008265; Lipase GDSL_AS.
DR Pfam; PF00657; Lipase GDSL; 1.
DR PROSITE; PS01098; LIPASE GDSL; SER; 2.
SQ SEQUENCE 488 AA, 5431 MW, 6BE12FF5CB0AC9C5 CRC64;
Query Match 33.4%; Score 841; DB 2; Length 488;
Best Local Similarity 44.5%; Pred. No. 61e-57;
Matches 185; Conservative 64; Mismatches 147; Indels 20; Gaps 9;
QY 34 LEPLGKSTLRLRAEMPTTCPTONEPFLTRPRNSNY-TYPIKPAIE---NWGSDFLCTE 89
DB 1 MEPAGEKDEPLSVKHGRPMKCSQSPYLFVSRYNSNYLTRLOKQDKLEVRGAEIRCPD 60
QY 90 WKASNSVPTSVHQLRADIKVVAALGDSLT--TAVGARPNNSSDLPTSWRGLSWISIGDG 147
DB 61 KQPSDVPTSVHRLKPADINVTIGALGDSLTAGNAGSTPGNVLVDLTQYRGLSVSGDE 120
QY 148 NLEHTHTLPLNKLKPNPILGFTSTWECT---AGLNVAAGARADMPAQAWDLVERMK 204
DB 121 NIGTVTTLANILREFNPSLKGFSVGTGKETSFNALQNAVAGRAEDLPVQARLVDLMK 180
QY 205 NSPDINLEKDWKLVTLFIGNDLCHYCNPEHAHLATEYVQHQALDILSELPRAFVNV 264
DB 181 NDTRIHFQEDWKIITLFIGNDLDCDFNDLVHYSFQNFDTNIGKALDILHAEPVPAFVNL 240
QY 265 VEVME---LASLYQGGGKCAMLAQNCTC-LRHSQSLSLEKQELKVNWNLQHGSISSFS 320
DB 241 VTVLEIVNRLRYQEKVYCFRMLRLSLCPVLKFDNDNSTELATLIEFNKKFQKXTHQLI 300
QY 321 YWQYTOREDFAVVQVQFFQNTLITPLNERGDTLTFSEDCPHSDRGHAEMAIALWNM 380
DB 301 ESGRYDTRDFVTVVQVFFENVDMPTKTEGLPDNSFPAPDFHFSKSHSRAASALWNM 360
QY 381 LEVGRKTTNNFTHSRALKKCPSPSPYLYTLRNS-----RLLPQAEAEPEVLY 431
DB 361 LEVPGQKTRHKF-ENKINITCPNQVQFFLRTYNSMQHGWTWLPDR-DRAPSALH 414
RESULT 6
ID Q8K255 PRELIMINARY; PRT; 186 AA.
AC Q8K255;
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE BC033606 protein.
GN Name=BC033606;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=FVB/N-3; TISSUE=Mammary tumor;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N-3; TISSUE=Mammary tumor;
RA Director MGC Project;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033606; AAH33606.1; ~;
DR MGD; MGI:2387632; BC033606.
SQ SEQUENCE 186 AA, 21471 MW, 56153A626A22315 CRC64;
Query Match 25.2%; Score 635; DB 2; Length 186;
Best Local Similarity 72.5%; Pred. No. 1.9e-41;
Matches 116; Conservative 18; Mismatches 26; Indels 0; Gaps 0;
QY 303 QELKKVNNLQHGSISSFSYWHQYTOREDFAVVQVQFFQNTLITPLNERGDTLTFSEDCP 362
DB 2 QELKKLNNLQSGISELSYWHYMERDFAVTVQVQFFFTFIPLNERGLDITFSEDCP 61
QY 363 HFSDRGHAEMAIALWNMLPEVGRKTTNNFTHSRALKKCPSPSPYLYTLRNSRLLPDQ 422
DB 62 YFSDRGHAEMAIALWNMLPEVGRKTTNNFTHSRALKKCPSPSPYLYTLRNSRLLPDQ 121
QY 423 AEAPEVLYWAVFVAVAGVLVVGIIQTVVWRCRRGRRED 462
DB 122 AEAPEVLYWAVFVAVAGVLVVGIIQTVVWRCRRGRRED 161
RESULT 7
ID O01300 PRELIMINARY; PRT; 374 AA.
AC O01300;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein F09C8.1.
GN ORFNames=F09C8.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]


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RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA McMurray A.A.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL, 268132; CA92221.2; -.
DR F01R, T20655; T20655.
DR WormBase; WBGene00008621; F09C8.1.
DR WormPep; F09C8.1; CE31470.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR001087; Lipase_GDSL.
DR Pfam; PF00657; Lipase_GDSL; 1.
KW Hypothetical protein.
SQ SEQUENCE 374 AA; 41921 MW; 553E0DB7EE3A41EC CRC64;

Query Match 24.4%; Score 613.5; DB 2; Length 374;
Best Local Similarity 38.4%; Pred. No. 2.3e-39;
Matches 132; Conservative 63; Mismatches 118; Indels 31; Gaps 8;

QY 91 KASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSDLPTSWRGLSWSIGDGNLE 150
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
35 KKSQVPTNVNSVRPADIKLIMALGDSLTAANGAGADPVAVLQYRGLAQAGGDKTLE 94

QY 151 THTLPNILKKNPYLLGFST-----STWEGTAGLNVAAGARMDPAQAWDLVERMN 205
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
95 EHVTPINLKKYIPDPVFGSYNGIGSPNWE-IARLNVAAMPANAKDLPGQARQLVQLIQ 153

QY 206 SPD-INLEKDWKLVTLFGVNDLCHYCENPEAHLATEYVQHIOQALDILSELPRAFNV 264
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
154 HTEVNMKEDWKLNIIFGNDICGCRKVEDSPYNCAQDIKQAVQIYDNNVRVIVSL 213

QY 265 VEVNELASLYQGGGK--CAMLAQNNTCLRHSQSSLEKOEKLVNMLQHGISSFSY 322
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
214 TGMHLMLRQTDIGHWFCQRL-HHDECGC--ESNKNFTDADIRQACVD-----Y 260

QY 323 HOYT-----QREDFAVVQPPQNTLPLNERGDTLTFPSEDCFHPSDRGHAME 373
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
261 NKYEKQIETDGFTEKNDFTYVQPMFQDTLIPPMENGKPTQKFFAPDCFHPSQNGHALVS 320

QY 374 IALNNMLPEVGRKTSNFTSHRAKLKCPSPESPLYVLTLSNR 417
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
321 TYLWNNILQPVGSKSTVSNMSPVLOTLACPDAAACPFIRTPKNSQ 364

RESULT 8
Q23119 PRELIMINARY; PRT; 382 AA.
AC Q23119
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein W02B12.1.
GN ORFNames=W02B12.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Swinburne J., Ainscough R.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL, 266521; CA91393.2; -.
DR F01R, T26083; T26083.
DR WormBase; WBGene00012201; W02B12.1.
DR WormPep; W02B12.1; CE03761.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR001087; Lipase_GDSL.
DR Pfam; PF00657; Lipase_GDSL; 1.
KW Hypothetical protein.
SQ SEQUENCE 382 AA; 41772 MW; 6430145BB8525CA3 CRC64;

Query Match 22.9%; Score 577.5; DB 2; Length 382;
Best Local Similarity 37.5%; Pred. No. 1.5e-36;
Matches 132; Conservative 56; Mismatches 143; Indels 21; Gaps 9;

QY 80 NWSDFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTTA--VGARPNNSSDLPTSWR 137
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
24 NWSCD--ASVMAKSKVPTSAHSVRPADIKVIGALGDSLTAANGAGAGQPGDPLAVILQYR 81

QY 138 GLSWSIGDGNLETHHTLTPNLIKKNPYLLGF-----STWEGTAGLNVAAGARADM 192
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
82 GLAFQIGGKSLDSEHTIVANVLRKNPTLVGASKIGSENWVE-VSHLMGVPGAESKID 140

QY 193 PAQAWDLVERMKNSPDINLEKDWKLVTLFGVNDLCHYCENP-----EAHLATEYVQHIQ 247
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
141 IGQARALVNTMHAISEINVKEDWKLNVIFIGANDICVYCEDPYFNSTALHGNATFEKNI 200

QY 248 QALDILSEELPRAFNVVEVMEELASLYQGGGK--CAMLAQNNTCLRHSQSSLEKOE 305
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
201 AAVQILQDNLPRITVSLTGMFNMRMLRKIDKKYFCGLHT-PECDC--ESNKTQTD 257

QY 306 KKVNNWNLQHGISSFSYWHQYTOREDFAVVQPPQNTL-TPLNREGDTLTFSEDCFHF 364
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
258 QGVCFGYNNAEKDIQNTGLFDNKDDFTFVQVQPPFNGLDPPYASGVVDMTFFAPDCFHF 317

QY 365 SDRGHAEATALNMMLEPVGRKTSNFTSHRAKLKCPSPESPLYVLTLSNR 416
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
318 SAYGHGNIHMLNTIIVQVGFKQTSVNLSDPSVGLHCPSTNCPPFTTKNS 369

RESULT 9
Q7Q5J6 PRELIMINARY; PRT; 348 AA.
AC Q7Q5J6
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AGCP5492 (Fragment).
GN Name=agCG53007; ORFNames=ENSANGG00000018581;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAA01008960; EAA11331.1; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR001087; Lipase_GDSL.
DR InterPro; IPR008265; Lipase_GDSL_AS.
DR Pfam; PF00657; Lipase_GDSL; 1.
DR PROSITE; PS01098; LIPASE_GDSL_SER; 1.
FT NON_TER 1
SQ SEQUENCE 348 AA; 39561 MW; F77477CB89FE7B9E CRC64;
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Query Match      22.9%; Score 575.5; DB 2; Length 348;
Best Local Similarity 39.8%; Pred. No. 28-36; Mismatches 132; Indels 19; Gaps 11;
Matches 137; Conservative 56;

Qy 85 FLC-TENKASNPVTSVHOLRPADIKVVAALGDSLTAVGARNNSDLPTSWRGLSWI 143
Db 12 FFCNTTGMRETSVPTSDVRLRPGDIDIIGAIGDSLTAGNAGMATNILEVLNKGLSWSI 71

Qy 144 GCGNLETHLTNLILKKNFYLLGFGSTSTWEGT--AGL-NVAAGARADMPAOWDLV 200
Db 72 GCGTWRQFTLTNLILKKNFYLLGFGSTSTWEGT--AGL-NVAAGARADMPAOWDLV 131

Qy 201 ERMKNSPDINLEKDWKLVTLFIGVNDLCH---YCNPEAHLATEYVQHIQQALDILSEEL 257
Db 132 KRMISDRKLDINNHWKMITLIMGDNFCABICYMATPE-KILQYHEKNIVSALRTFRDYL 190

Qy 258 PRAFVNVV--EVMELASLYQGGKGCAMLAQNNCTCLRHSSQSLSEKQELKKV--NWN-L 312
Db 191 PRTFVNLAASPKVDILARFKNKPQECVSMHV-IECPCLLATRFRKQERFRVKLIEDWNML 249

Qy 313 QHGSSSYWHQYTOREDFAVVQPFQNTLTPLNERGDTDLTFFSDECFHFSDRGHAEM 372
Db 250 QMDIAAREEFH---RKPDFAVVYQFTWNLTFFETASGDDTFYMSLDCEHLKQGYALA 306

Qy 373 AIALWNNMLEPVGRKTTNNFTHSRALKCPSPESPILYTLRNS 416
Db 307 SNALWNNMLEPVGGK--SMNWEREFTLFRCPSEAMPFLRTPGNS 348

RESULT 10
Q7PI39 PRELIMINARY; PRT; 331 AA.
AC Q7PI39;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DE ENSANGP0000025054 (Fragment).
GN Name=ENSANG0000019814;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAB01008956; EAA44293.1;
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR001087; Lipase_GDSL.
DR Pfam; PF00657; Lipase_GDSL; 1.
FT NON_TER 1
FT SEQUENCE 331 AA; 37931 MW; 9872EBF521D706D CRC64;
SQ
Query Match      22.4%; Score 563; DB 2; Length 331;
Best Local Similarity 39.4%; Pred. No. 1.7e-35;
Matches 132; Conservative 54; Mismatches 133; Indels 16; Gaps 8;

Qy 93 SNSVPTSVHOLRPADIKVVAALGDSLTAVGARNNSDLPTSWRGLSWISIGDGNLETH 152
Db 2 SAKVPTSVHOLRPADIKVVAALGDSLTAVGARNNSDLPTSWRGLSWISIGDGNLETH 61

Qy 153 TTLNLILKKNFYLLGFGSTSTWEGT--AGL-NVAAGARADMPAOWDLVEMKNSPDI 209
Db 62 TTLNLILKKNFYLLGFGSTSTWEGT--AGL-NVAAGARADMPAOWDLVEMKNSPDI 121

Qy 210 NLEKDWKLVTLFIGVNDLCH---YCNPEAHLATEYVQHIQQALDILSEELPRAFNVYE 266
Db 122 DWKRDWKLVTIAGNDICVSCVTWRYPE-QLPAKHLRLQRTLYLRDSMPRTFVNLVS 180

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Qy 267 VMLAS--LYQGGGKGCAMLAQNNCTC---LRHSQSSLEKQELKKVNNLQHGISSFSY 321
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Qy 322 WHOYTQREDFAVVQPFQNTLTPLNERGDTDLTFFSDECFHFSDRGHAEMAIALWNNML 381
Db 240 SREFRGLDEFAVVYQWLSNVTVMKNGK-DIDYSLLSYDCFHMSQKGNAGAFALTALWNNML 298

Qy 382 EPVGRKTTNNFTHSRALKCPSPESPILYTLRNS 416
Db 299 EPVGKKT--NWRPLLKNFKCPTKESPYLITYDNS 331

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AC Q7PCU2;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
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GN Name=agCG44667; Synonym=agCG45512; ORFNames=ENSANG0000012533;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAB01008916; EAA09798.1;
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR001087; Lipase_GDSL.
DR Pfam; PF00657; Lipase_GDSL; 1.
SQ SEQUENCE 373 AA; 42957 MW; C31C5B6C99A164B1 CRC64;

Query Match      22.2%; Score 560; DB 2; Length 373;
Best Local Similarity 36.8%; Pred. No. 3.5e-35;
Matches 149; Conservative 46; Mismatches 144; Indels 66; Gaps 12;

Qy 34 LEPLGSKTETDLRAEMPTCTQNEPFLRTPRNSNTYPIKPALENWGSDFLCWEMKAS 93
Db 13 LGPTGMRDEGVSLQARVP-----PNVPPFCDVGRVY-----S 44

Qy 94 NSVPTSVHOLRPADIKVVAALGDSLTAVGARNNSDLPTSWRGLSWISIGDGNLETH 153
Db 45 STPTSVHOLRPADIKVVAALGDSLTAVGARNNSDLPTSWRGLSWISIGDGNLETH 104

Qy 154 TPLNLILKKNFYLLGFGSTSTWEGT--AGL-NVAAGARADMPAOWDLVEMKNSPDI 210
Db 105 TPLNLILKKNFYLLGFGSTSTWEGT--AGL-NVAAGARADMPAOWDLVEMKNSPDI 164

Qy 211 LEKDWKLVTLFIGVNDLCH---YCNPEAHLATEYVQHIQQALDILSEELPRAFNV 262
Db 165 WHKHWKLLTLMIGNDICVSCVTWRYPE-QLPAKHLRLQRTLYLRDSMPRTFVNLVS 219

Qy 263 NVV--EVMELA-SLYQGGGKGCAMLAQNNCTC---LRHSQSSLEKQELKKVNNL 311
Db 220 NLVPSPLINLSFSDIKVQAPLTCQFVRPIECSCLYGPKYSNGRNLRYQLERRFKV 274

Qy 312 LQHGSSSYWHQYTOREDFAVVQPFQNTLTPLNERGDTDLTFFSDECFHFSDRGHAEM 371
Db 275 IMERVSHRPFHS---DDFTVYVQPFYRDASIFHRRDGKPDLSIWAIDCVHLSQKHAV 330

Qy 372 MAJALWNNMLEPVGRKTTNNFTHSRALKCPSPESPILYTLRNS 416
Db 331 SANGLWNNMLEPETHKTTV--LKLQFEEPCPTPENPYIKTYNS 373

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		Query Match	22.2%	Score 559.5;	DB 2;	Length 398;
		Best Local Similarity	35.5%;	Pred.No. 4.le-35;		
		Matches 129;	Conservative 61;	Mismatches 130;	Indels 43;	Gaps 11;
Qy	90	WKASNSVPTSVHQLRPADIKVVAALGDSLTTAVCARPNNSDLPT--SWRGLSWSIGDGD	147			
		: : : : : : : : :				
Dd	34	YKKSQQVPTSASHVSRESFKIIGALGDSLTAAGACAPKGDPFLAVILQYRGFLAFCQGDS	93			
Qy	148	NLEHTYT-----LPNLLKKENPYLLGGST-----STWEGTAGLN	181			
		: : : : : : : :				
Dd	94	SLDEHYTVASENFNLNLEQTSAPAIMOLLADVKKFSPNIMGYSTGIGSANVWE-VSKLN	152			

RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.	
RL	[8]	
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RP	STRAIN=Bristol N2;	
RA	Waterston R.;	
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.	
RL	[9]	
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RP	STRAIN=Bristol N2;	
RA	Waterston R.;	
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.	
RL	[10]	
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RP	STRAIN=Bristol N2;	
RA	Waterston R.;	
RL	Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.	
RL	[11]	
RN	SEQUENCE FROM N.A.	
RP	STRAIN=Bristol N2;	
RA	Waterston R.;	
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.	
RL	[12]	
RN	SEQUENCE FROM N.A.	
RP	STRAIN=Bristol N2;	
RA	Waterston R.;	
RL	Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.	
RL	[13]	
RN	SEQUENCE FROM N.A.	
RP	STRAIN=Bristol N2;	
RA	Waterston R.;	
RL	Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.	
RL	EMBL: AC024847; AAF60857.1; -	
DR	WormBase: WBGene00022040; Y65B4BR.1.	
DR	WormPep; Y65B4BR.1; CE25539.	
DR	GO: GO:0003844; F: catalytic activity; IEA.	
DR	InterPro: IPR001087; Lipase_GDSL.	
DR	Pfam: PF00657; Lipase_GDSL; 1.	
DR	Hypothetical protein.	
KW	SEQUENCE 377 AA; 2A93D3842C80E6A5 CRC64;	
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	Matches 132; Conservative 59; Mismatches 131; Indels 46; Gaps 11;	
QY	72 YPIKPAIENWGSDFLCTEWKASNSVPTSVHQLRPADIKVVAALGDSLTTAVGARPNNSSD 131	
DB	24 YP-----GWQCD--ASLYQSKXNPTSAHSVRFTDIKVLGALGDSLTAANGAGAPKGP 75	
QY	132 LPT--SWTGLSWSIGDGNLEHTHTLPILAKPEPYLLGFST-----STWEGTAGLNVA 184	
DB	76 LAVILQYRGLAFQCGGDSLDEHVTAVANVLKFPSPNLNGYSTGIGSANVWE-VSKLNQAV 134	
QY	185 EGARADMPAQAWDIVERMKNSPDINLEKDWKLVTFTGVNDLCHYCENPE--AHILATEY 242	
DB	135 PGAEAIIDITQARALVQIIQSHKEIDYKTDWKLINVFIGANDMCAVCNDRENGPHSKAIW 194	
QY	243 VQHIQOALDILSEELPRAFVNVVFWELASLYQGOGGK--CAMLAQANNCTCLRHSQSSL 300	
DB	195 KQNVITAIQILKDNLPRTTVSMGTGFMDFMAMLRQIDHDHDKYFCDLGHV-FECPCEKNDKP- 252	
QY	301 EKQELKKVNNLQHGISFSFSYHVOYQTRP-----DFAVVVQPPFQN-TLTPLINE 348	
DB	253-----NTDISAACHLYMDAQOEIQDSGIFDSTDDFTFVVQPPFNGITVPPLKP 300	
QY	349 RGPDTLTFSSDCFHFSDRGHAMATALNNNMLEPVGKRTTSNNFTHSPAKLKCPSPEP 408	
DB	301 DGEVNLWDWPA DCFHF SKLGHANVAKHLWNNIVQPVGSKHQNLNSDPTIPLNCDDTKCP 360	
QY	409 YLTLRNS 416	
DB	361 FFRFTKNS 368	

Search completed: March 25, 2005, 14:36:23
Job time : 184 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 11:21:05 ; Search time 4150.02 Seconds
(without alignments)
11092.094 Million cell updates/sec

Title: US-09-778-961-3_COPY_12201_13150
Perfect score: 950
Sequence: 1 taatcataaacacttcttgga.....atggttaattccattgatt 950

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	950	100.0	43543	6	AX711964 Sequence
2	922	97.1	180465	9	AC074011 Homo sapi
3	216.2	22.8	217253	2	AC102372 Mus muscu
4	204.6	21.5	214038	2	AC141490 Rattus no
5	70	7.4	265	6	AX417822 Sequence
6	70	7.4	1790	9	BC042674 Homo sapi
7	70	7.4	1835	6	AX711962 Sequence
8	70	7.4	3648	6	AX417817 Sequence
9	70	7.4	4377	6	AX492941 Sequence
10	67	7.1	1776	6	C0715991 Sequence
11	66.8	7.0	608	6	AX417821 Sequence
12	55.4	5.8	4590	10	D63648 Rattus norv
13	55.4	5.8	4608	10	AF045454 Cavia por
14	55.4	5.8	4613	6	E13935 Rat mRNA fo
15	50.6	5.3	4612	4	Z12841 O. cuniculus
16	50.2	5.3	281723	3	AF929359 Plasmodiu
17	46	4.8	247026	2	AC097342 Rattus no
18	46	4.8	278699	2	AC136847 Rattus no
19	44.4	4.7	256946	2	AC097848 Rattus no

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	23	42.6	4.5	176704	2	CR628364	Danio rer
	24	42.6	4.5	182337	2	AC135881	Rattus no
	25	42.6	4.5	190930	2	EX936353	Danio rer
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	27	42.6	4.5	208866	5	AC144711	Danio rer
c	28	42.6	4.5	214611	2	BX927254	Danio rer
	29	42.6	4.5	221163	2	BX572628	Danio rer
c	30	42.6	4.5	223363	2	EX957302	Danio rer
	31	42.6	4.5	257477	2	AC106951	Rattus no
	32	42.6	4.5	200176	5	EX005442	Zebrafish
c	33	42.6	4.5	258091	5	EX571981	Zebrafish
	34	41.8	4.4	168347	9	AC079756	Homo sapi
c	35	41.6	4.4	12123	8	AV150645	Zea mays
	36	41.6	4.4	191042	2	AY560576	Zea mays
	37	41.2	4.3	160603	8	AC084818	Oryza sat
	38	41	4.3	88044	8	AC145780	Oryza sat
	39	41	4.3	125020	9	AF429315	Homo sapi
	40	41	4.3	165715	2	CR759743	Danio rer
c	41	41	4.3	184033	2	CR759896	Danio rer
c	42	41	4.3	198052	5	AL954192	Zebrafish
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ALIGNMENTS

RESULT 1
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LOCUS AX711964 43543 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 3 from Patent WO02062977.
ACCESSION AX711964
VERSION AX711964.1 GI:29787749
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Yan, C., Ketchum, K., di Francesco, V. and Beasley, E. M.
TITLE Human phospholipase b-like polypeptide and uses thereof
JOURNAL Patent: WO 02062977-A 3 15-AUG-2002;
PE Corporation (NY) (US)
FEATURES
Location/Qualifiers
source
1. 43543
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Qy	61	AATTACAAAGCCAAAGAAATAGATAGT	100.0%	950;	0;	0;	0;	0;
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Mon Mar 28 09:43:28 2005

Direct Submission
Submitted (09-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 180465)
Waterston,R.
Direct Submission
Submitted (09-AUG-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 180465)
Waterston,R.
Direct Submission
Submitted (07-NOV-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Aug 9, 2001 this sequence version replaced gi:13431259.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics

Center project name: H_NH0780J06

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RP11-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E.,
Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)

VECTOR: pBAC3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is AC022076. Actual start of this
clone is at base position 1 of RP11-780J6; actual end is at base
position 180465 of RP11-780J6.

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/rpt_family="MIR"
3140..3189
repeat_region
repeat_region
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repeat_region

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12441 TTTATACAGTCTCTTTCTATATAGTCGAGAGATCATGTTAAATAATCTACAGGCGAG 12500
301 GATGTAGTCTTTCTCTCTCAAGCAAACTTCAGTCTGTCAGATAACTTCTCCATGT 360
12501 GATGTAGTCTTTCTCTCTCAAGCAAACTTCAGTCTGTCAGATAACTTCTCCATGT 12560
361 GTTTTTTTTTCTTTAGATAGCCCTTCTGAGAACCCCTCGGAATAGTAACTACAGC 420
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13041 GGAAGTGGAGGAGGCTGTTCTATGTTCTGTTGGGCCCTTAGGCTTGTGTTGTTCAAGTC 13100
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RESULT 2
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DEFINITION AC074011
ACCESSION AC074011
VERSION AC074011.5 GI:15144519
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 180465)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 180465)
AUTHORS Paulson, E., Cotton, M. and Lohmeyer, A.
TITLE The sequence of Homo sapiens BAC clone RP11-780J6
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 180465)
AUTHORS Waterston, R.H.

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Mon Mar 28 09:43:28 2005

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 AC102372
 AC102372:2 GI:30018075
 HTG: HTGS_PHASE1; HTGS_DRAFT.
 KEYWORDS
 SOURCE Mus musculus (house mouse)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 1 (bases 1 to 217253)
 Birren, B., Nusbaum, C. and Lander, B.
 Mus musculus, clone RP23-262J12
 Unpublished
 2 (bases 1 to 217253)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
 Anderson, S., Barna, N., Bastien, V., Boguslavskiy, L., Boukhgalter, B.,
 Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
 Choepel, Y., Colangelo, M., Collins, S., Collamore, A., Cook, A.,
 Cooke, P., DeArelano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
 Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
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 Jones, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K.,
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 Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
 Roman, J., Roberti, M., Roy, A., Santos, R., Schauer, S., Schuback, R.,
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 Topham, K., Travers, M., Travis, N., Trigglio, J., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 217253)

RESULT 3
 AC102372
 LOCUS
 DEFINITION
 Mus musculus clone RP23-262J12, WORKING DRAFT SEQUENCE, 10
 unordered pieces.
 AC102372
 AC102372:2 GI:30018075
 HTG: HTGS_PHASE1; HTGS_DRAFT.
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 217253)
 Birren, B., Nusbaum, C. and Lander, B.
 Mus musculus, clone RP23-262J12
 Unpublished
 2 (bases 1 to 217253)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
 Anderson, S., Barna, N., Bastien, V., Boguslavskiy, L., Boukhgalter, B.,
 Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
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 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 217253)

AUTHORS
 Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
 Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
 Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
 Collamore, A., Cook, A., Cooke, P., Corum, B., DeArelano, K.,
 Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
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 Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (23-APR-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Apr 17, 2003 this sequence version replaced gi:17061458.
 All repeats were identified using RepeatMasker.
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L18594
 Center clone name: 262_J_12

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 10 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
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 * This record will be updated with the finished sequence
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us-09-778-961-3_copy_12201_13150.rge

Mon Mar 28 09:43:28 2005

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Direct Submission
Unpublished
2 (bases 1 to 214038)
Worley,K.C.
Direct Submission
Submitted (17-MAR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 214038)
Worley,K.C.
Direct Submission
Submitted (18-MAR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Mar 18, 2003 this sequence version replaced gi:28975751.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KEHN
Center clone name: CH230-188E12
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 193611 bases at least Q40
Consensus quality: 200661 bases at least Q30
Consensus quality: 204826 bases at least Q20
Estimated insert size: 193990; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 62 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
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* This record will be updated with the finished sequence
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Query Match 21.5%; Score 204.6; DB 2; Length 214038;
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Db 44448 TTTGTCCTCTCTGTTTAAACAGCACTCACAGAACCCCTTCGGGAAGGACTGAATTC 44389
Qy 240 GTTTATACAGTTCTTTCTATATAAGTCAGAGAATCATGTTAAATAAATCTACAGGGCA 299
Db 44388 GTCTATGAGCTCTTTCACATCAATGC---AGAGCCCTGTTAGGAGACTAGAGGCA 44332
Qy 300 GGATGTTAGTTTCTCTCTCTCAAGCAAACTTCAGTGTGTGACATAAATCTTCCATG 359
Db 44331 GCAGGG-----TGCTGAGCTCATCGGCAGCCCTCATGTTAGATAAATCTGTGCG 44282
Qy 360 TGTCTTTTCTCTTAGAATGAGCCCTTCTGAGAACCCCTCGGAATAGTAATACAC 419
Db 44281 -ATTCTCTTCTCTTAGGACAAGCCCTTCTGAGAACCTTTCGGGAACAGTAATACAC 44223
Qy 420 GTACCCCATCAAGCCAGCCATAGAGTAACCCCTGACTCACATCTGCTCTCTCAGACAC 479
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Qy 480 AAACCATTTCCACCTGCCAGGGGCTCGGGTGTGTGACAGTTTACAGATATTCACAGAAG 539
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Qy 588 TCCGGACCAAGAACCCAGGATTTCTTAAACATGTTCTCAAGTTGCTTACCTGACGTC 647
Db 44042 GATCGGAACTAAGCCCCCAGAGTAGTCTGACATGTTCTCAGTTGCTTACCTGACGTC 43983
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Db 43982 AGTGGCCAAAGCAGAGGAAGTG -CTGGGATCATGTGCACTGACCTT-----TGATGTCC 43930
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Db 43929 TCAGAGAGCTGTTGTTTTTAAATTAACAGCTTAGCCTTACAGAGTGTGAGATAGCGGATAAG 43870
Qy 768 GATGTGGCTGTGACTTCTTGAAGCTGAGGCTGAGTGGGAGGAACCTACAAATCTTGGG 827
Db 43869 GAGAGTGGGTATTAGTGTTCAGGTGGGGCAGGGGGCATGAAGTGCCCACTTCTCTG 43810
Qy 828 ATGGGACCCAAA 840
Db 43809 AAGTGAACCCCTAA 43797
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RESULT 5

AX417822
LOCUS AX417822 Sequence 6 from Patent WO0231161. 265 bp DNA linear PAT 18-JUN-2002
DEFINITION AX417822
ACCESSION AX417822
VERSION AX417822.1 GI:21522940

KEYWORDS

Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Zhu, Z.

TITLE Regulation of human phospholipase-like enzyme
JOURNAL Patent: WO 0231161-A 6 18-APR-2002;
BAYER AG (DE)

FEATURES

source
1..265
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 7.4%; Score 70; DB 6; Length 265;
Best Local Similarity 93.6%; Pred. No. 2.9e-09;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 367 TTTTCTCTTAGAATGAGCCCTTCTGAGAACCCCTCGGAATAGTAATACACGTACCC 426
Db 91 TGTCCCACTCAGATGAGCCCTTCTGAGAACCCCTCGGAATAGTAATACACGTACCC 150
Qy 427 ATCAAGCCAGCCATTGAG 444
Db 151 ATCAAGCCAGCCATTGAG 168

RESULT 6

BC042674
LOCUS BC042674 1790 bp mRNA linear PRI 03-FEB-2004
DEFINITION Homo sapiens phospholipase B1, mRNA (CDNA clone MGC:35447
IMAGE:5191712), complete cds.

ACCESSION

BC042674

VERSION

BC042674.1 GI:27503748

KEYWORDS

MGC.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 1790)

AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Dietzenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soarsina, K., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S.,
Carroll, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center

Mon Mar 28 09:43:28 2005

Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: ang@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 50 Row: k Column: 10.

FEATURES

source
1. .1790
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="Brain, adult, 6 pooled whole brains"
/clone_id="NIH_MGC_114"
/lab_host="DH10B"
/notes="vector: pCMV-SPORT6"

gene

1. .1790
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/note="synonyms: FLJ30866, PLB"
/db_xref="LocusID:151056"
196-1467
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/codon_start=1
/product="PLB1 protein"
/protein_id="AAH42674.1"
/db_xref="GI:27503749"
/db_xref="LocusID:151056"
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MELASLYOCQGGKAMLAQNNCTCLRHSSSLEKOLKVVNNLOHGISSFSYWHQY
TORDEFVAVVQFFQNTLTPLNREGDIDLTFSEDCFHSDRGHAEWALANNMLEP
VCRKTSNNFTHSRAKLCPSPSPYLTILNSRLLPDQAEAPVULYVNAVPAVG
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CDS

379-1176
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Lipase/Acylhydrolase"
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misc_feature

379-1176
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Lipase/Acylhydrolase"
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ORIGIN

Query Match 7.4%; Score 70; DB 9; Length 1790;
Best Local Similarity 93.6%; Pred. No. 3.6e-09;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 367 TTTTCTCTTAGAATGAGCCCTTCTGAGAACCCCTCGGAATAGTAACACGTAACCC 426
DB 208 TGTCCTCACTCAGAAATGAGCCCTTCTGAGAACCCCTCGGAATAGTAACACGTAACCC 267
QY 427 ATCAAGCCAGCCATTGAG 444
DB 268 ATCAAGCCAGCCATTGAG 285

RESULT 7

AX711962 LOCUS 1835 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1 from Patent WO02062977.
ACCESSION AX711962
VERSION AX711962.1 GI:29787748
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Yan, C., Ketchum, K., di Francesco, V. and Beasley, E.M.
Human phospholipase b-like polypeptide and uses thereof

JOURNAL Patent: WO 02062977-A 1 15-AUG-2002;
PE Corporation (NY) (US)
FEATURES Location/Qualifiers
source 1. .1835
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 7.4%; Score 70; DB 6; Length 1835;
Best Local Similarity 93.6%; Pred. No. 3.6e-09;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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DB 335 TGTCCTCACTCAGAAATGAGCCCTTCTGAGAACCCCTCGGAATAGTAACACGTAACCC 394
QY 427 ATCAAGCCAGCCATTGAG 444
DB 395 ATCAAGCCAGCCATTGAG 412

RESULT 8

AX417817 LOCUS 3648 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 1 from Patent WO0231161.
ACCESSION AX417817
VERSION AX417817.1 GI:21522937
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Zhu, Z.
Regulation of human phospholipase-like enzyme
Patent: WO 0231161-A 1 18-APR-2002;
BAYER AG (DE)
FEATURES Location/Qualifiers
source 1. .3648
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 7.4%; Score 70; DB 6; Length 3648;
Best Local Similarity 93.6%; Pred. No. 3.9e-09;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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DB 2401 TGTCCTCACTCAGAAATGAGCCCTTCTGAGAACCCCTCGGAATAGTAACACGTAACCC 2460
QY 427 ATCAAGCCAGCCATTGAG 444
DB 2461 ATCAAGCCAGCCATTGAG 2478

RESULT 9

AX492941 LOCUS 4377 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 1 from Patent WO02059328.
ACCESSION AX492941
VERSION AX492941.1 GI:23338611
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Turner Jr, C.A., Miranda, M. and Yu, X.
Human lipase and polynucleotides encoding the same
Patent: WO 02059328-A 1 01-AUG-2002;
JOURNAL

LEXICON GENETICS INC (US)
Location/Qualifiers
1. 4377
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
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Best Local Similarity 93.6%; Pred. No. 3.9e-09;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 367 TTTTCTCTTAGAATGAGCCCTTCTCGAAGACCCCTCGGAATAGTAACACTACGATACCCC 426
Db 3118 TGTCCCACTCAGATGAGCCCTTCTCGAAGACCCCTCGGAATAGTAACACTACGATACCCC 3177
Qy 427 ATCAAGCCAGCCATTGAG 444
Db 3178 ATCAAGCCAGCCATTGAG 3195

RESULT 10
LOCUS CQ715991 1776 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 1925 from Patent WO02068579.
ACCESSION CQ715991
VERSION CQ715991.1 GI:42276848
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 1925 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 975 GAATGAGCCCTTCTCGAAGACCCCTCGGAATAGTAACACTACGATACCCCATCAAGCCAGC 1034
Qy 438 CATTGAG 444
Db 1035 CATTGAG 1041

RESULT 11
AX417821
LOCUS AX417821 608 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 5 from Patent WO0231161.
ACCESSION AX417821
VERSION AX417821.1 GI:21522939
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Zhu, Z.
TITLE Regulation of human phospholipase-like enzyme

JOURNAL Patent: WO 0231161-A 5 18-APR-2002;
BAYER AG (DE)
Location/Qualifiers
1. 608
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Best Local Similarity 91.0%; Pred. No. 2.8e-08;
Matches 71; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 367 TTTTCTCTTAGAATGAGCCCTTCTCGAAGACCCCTCGGAATAGTAACACTACGATACCCC 426
Db 475 TGTCCCACTCAGATGAGCCCTTCTCGAAGACCCCTCGGAATAGTAACACTACGATACCCC 534
Qy 427 ATCAAGCCAGCCATTGAG 444
Db 535 ATCAAGCCAGCCATTGAG 552

RESULT 12
D63648
LOCUS D63648 4590 bp mRNA linear ROD 01-NOV-2000
DEFINITION Rattus norvegicus mRNA for phospholipase B, complete cds.
ACCESSION D63648
VERSION D63648.1 GI:2696235
KEYWORDS phospholipase B.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (sites)
AUTHORS Takemori, H., Zolotaryov, P.N., Ting, L., Urbain, T., Komatsubara, T., Hatano, O., Okamoto, M. and Tojo, H.
TITLE Identification of functional domains of rat intestinal phospholipase B/lipase. Its cDNA cloning, expression, and tissue distribution
JOURNAL J. Biol. Chem. 273 (4), 2222-2231 (1998)
MEDLINE 98113187
PUBMED 9442065
REFERENCE 2 (bases 1 to 4590)
AUTHORS Tojo, H.
TITLE Direct Submission
JOURNAL Submitted (22-JUL-1995) Hiromasa Tojo, Osaka University Medical School, Molecular Physiological Chemistry; 2-2 Yamada-oka, Suita, Osaka 565, Japan (E-mail:htojo@mr-mbio.med.osaka-u.ac.jp, Tel:06-879-3283(ex.3283), Fax:06-879-3288)
Location/Qualifiers
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36. 4388
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ORIGIN

Query Match 5.8%; Score 55.4; DB 10; Length 4590;
Best Local Similarity 84.9%; Pred. No. 8.6e-05;
Matches 62; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 372 CTCTTAGAATGAGCCCTTCTGAGAACCCCTCGGATAGTAACACGATACCCCATCAA 431
Db 3170 CACCAAGGACAAAGCCCTTCTGAGAACCTTCCGGAACAGTAACATACGATACCTATCAA 3229

Qy 432 GCCAGCCATTGAG 444
Db 3230 GCCAGCCATTGAG 3242

RESULT 13
AF045454 Cavia porcellus phospholipase B (PLB) mRNA linear ROD 02-JUN-1998
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

REFERENCE
AUTHORS
TITLE
JOURNAL
SUBMITTED (30-JAN-1998) INSERM unite 326, Hopital Purpan, Toulouse 31059, France

FEATURES
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1. .4608
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/mol_type="mRNA"
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ORIGIN

Query Match 5.8%; Score 55.4; DB 10; Length 4608;
Best Local Similarity 84.9%; Pred. No. 8.6e-05;
Matches 62; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 372 CTCTTAGAATGAGCCCTTCTGAGAACCCCTCGGATAGTAACACGATACCCCATCAA 431
Db 3159 CACCAAGGAGAGCCCTTCTGAGAACCCCAAGACGAGCTACGATACCCCAACAA 3218

Qy 432 GCCAGCCATTGAG 444
Db 3219 GCCAGCCATTGAG 3231

RESULT 14
E13935 Rat mRNA for phospholipase.
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 4613)
Tojo, H. and Hasegawa, A.
NEW PHOSPHOLIPASE AND DNA CODING THE SAME
Patent: JP 1997248190-A 1 22-SEP-1997;
TOJO HIROMASA, TONEN CORP
OS Rattus sp. (rat)
PN JP 1997248190-A/1
PD 22-SEP-1997
PF 15-MAR-1996 JP 1996086022
PI TOJO HIROMASA, HASEGAWA AKIRA
PC C12N15/09, C07H21/04, C07K14/47, C12N5/10, C12N9/16, PC
C12N9/20//A61K38/46,
PC (C12N5/10, C12R1:91), (C12N9/16, C12R1:91), (C12N9/20, C12R1:91);
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CC topology: Linear;
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FT CDS 36. .4397

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 Db 3170 CACCAGACAGACGCTTCTCTGAGAACCTTCGGAGACAGTAACTACAGTACCCATACAA 3229
 Qy 432 GCCAGCCATTGAG 444
 Db 3230 GCCAGCCATTGAG 3242

RESULT 15
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 LOCUS O.cuniculus mRNA for phospholipase. 4612 bp mRNA linear MAM 09-JUN-1994
 DEFINITION
 ACCESSION Z12841
 VERSION Z12841.1 GI:1689
 KEYWORDS phospholipase.
 SOURCE Oryctolagus cuniculus (rabbit)
 ORGANISM Oryctolagus cuniculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 REFERENCE 1
 AUTHORS Boll, W., Schmid-Chanda, T., Semenza, G. and Mantei, N.
 TITLE Messenger RNAs expressed in intestine of adult but not baby rabbits. Isolation of cognate cDNAs and characterization of a novel brush border protein with esterase and phospholipase activity
 J. Biol. Chem. 268 (17), 12901-12911 (1993)
 JOURNAL 93286138
 MEDLINE
 PUBMED 8509424
 REFERENCE 2 (bases 1 to 4612)
 AUTHORS Boll, W.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-1992) WERNER BOLL, Dept. of Biochemistry 11,
 Swiss Federal Institute of Technology, ETH Zentrum,
 Universitaetsstrasse 16, Zuerich, CH-8092, Switzerland
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 polyA_site 4612
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 Db 3207 GCCAGCCGTCGAG 3219

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 Job time : 4156.02 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 08:45:20 ; Search time 494.725 Seconds
(without alignments)
11367.434 Million cell updates/sec

Title: US-09-778-961-3_COPY_12201_13150

Perfect score: 950
Sequence: 1 taatcatacacattcttggg.....atggttaattccattggatt 950

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

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- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	950	100.0	43543	6	ABQ82235 Human pho
2	70	7.4	265	6	AAD37413 Human pho
3	70	7.4	572	4	AAL01390 Human rep
4	70	7.4	572	4	ABL96843 Human tes
5	70	7.4	802	4	AH99765 Human pro
6	70	7.4	802	4	ABA08297 Human pho
7	70	7.4	1835	6	ABQ82234 Human pho
8	70	7.4	3648	6	AAD37410 Human pho
9	70	7.4	4268	6	ABX97048 Human NOV
10	70	7.4	4268	12	ADH42426 Novel hum
11	70	7.4	4268	12	ADN61812 Human CDN
12	70	7.4	4311	12	ADH13733 Human ENZ
13	70	7.4	4377	6	ABQ77623 Human lip
14	70	7.4	4377	6	ABQ77624 Human lip
15	70	7.4	4424	8	AAD52634 Human lip
16	70	7.4	4425	6	ABX97050 Human NOV
17	70	7.4	4425	12	ADH42430 Novel hum
18	70	7.4	4425	12	ADN61816 Human CDN
19	70	7.4	4508	12	ADO18836 Human lip
20	70	7.4	4512	12	ADO18837 Human lip

21	70	7.4	4607	8	AAD52626 Human lip
22	66.8	7.0	608	6	AAD37412 Human pho
23	55.4	5.8	4613	2	AAT91874 Rat phosp
24	43.2	4.5	2000	8	ADA71938 Rice gene
25	41.6	4.4	5506	10	ADC29909 FIE prote
26	41.6	4.4	13031	11	ADM39442 Maize Zmf
27	40.6	4.3	110000	5	AAF84800 Nucleotid
28	39.4	4.1	507	10	ADF01878 Bacterial
29	38.6	4.1	816	8	ACA30331 Prokaryot
30	38.4	4.0	14920	6	ABN80147 Human che
31	38.2	4.0	37256	12	ADQ97755 Human can
32	38	4.0	2031	10	ADA53206 Human cod
33	38	4.0	8113	4	ABL06899 Drosophil
34	38	4.0	37322	4	ABL06898 Drosophil
35	37.8	4.0	285	10	ADF01482 Bacterial
36	37.4	3.9	392	4	AAI85371 Human pol
37	37.4	3.9	424	8	ABX49621 Bovine ES
38	37.4	3.9	13712	6	ABL33531 Human imm
39	37.2	3.9	9733	6	ABL32682 Human imm
40	36.8	3.9	900	5	AAH74688 Nucleotid
41	36.8	3.9	900	5	AAH74677 Nucleotid
42	36.8	3.9	900	5	AAH74678 Nucleotid
43	36.8	3.9	900	5	AAH74676 Nucleotid
44	36.8	3.9	900	5	AAH74689 Nucleotid
45	36.8	3.9	900	5	AAH74686 Nucleotid

ALIGNMENTS

RESULT 1
ABQ82235
ID ABQ82235 standard; DNA; 43543 BP.
AC ABQ82235;
XX

DT 16-DEC-2002 (first entry)

DB Human phospholipase protein encoding DNA SEQ ID NO:3.

KW Human; phospholipase; enzyme; chromosome 2; gene; ds.

XX Homo sapiens.

XX Location/Qualifiers

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FT CDS 3000..41338

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FT /*product= "phospholipase"

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FT exon 3000..3098

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FT intron 3099..4565

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FT /*standard_name= "single nucleotide polymorphism (SNP)"

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Matches 950; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	12261	AATTACAAAGCCAAAGAAATAGATAGTCTCAGGATTAGGAGCTGTTTCACTTCTCTAGGA	12320
Qy	121	GGAAACACAAAGCAGACCCAGACTACAAATGGGTATGAAACCTCTGCAAGCCTTTTG	180
Db	12321	GGAAACACAAAGCAGACCCAGACTACAAATGGGTATGAAACCTCTGCAAGCCTTTTG	12380
Qy	181	TTGTCCATCCCTTCCAAAGCTGTTATGTAACCCCTCCGGGGAAATGAATGAATATG	240
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Qy	301	GATTGTAGTTTTTCTCCTCTCAAGCAAACTTCAGTGTCTGCAGATAAATCTTCCCATGT	360
Db	12501	GATTGTAGTTTTTCTCCTCTCAAGCAAACTTCAGTGTCTGCAGATAAATCTTCCCATGT	12560
Qy	361	GTGTTTTTTTCTTCTAGAAATGAGCCCTTCTGAGAACCCCTCGGAATAGTAACACG	420
Db	12561	GTGTTTTTTTCTTCTAGAAATGAGCCCTTCTGAGAACCCCTCGGAATAGTAACACG	12620
Qy	421	TACCCCATCAAGCCAGCATTTAGGTAACTTCACTCACTCACTCTCTCTCAGACACA	480
Db	12621	TACCCCATCAAGCCAGCATTTAGGTAACTTCACTCACTCACTCTCTCTCAGACACA	12680
Qy	481	AACCAATTTCCACCTGCCAGGGGCTCGGGTGTGGTACAGGTTTCAGAGTATTCACCTGAAGC	540
Db	12681	AACCAATTTCCACCTGCCAGGGGCTCGGGTGTGGTACAGGTTTCAGAGTATTCACCTGAAGC	12740
Qy	541	AGAAATGTACTTCTTACATCTGGGGATTTGGAATGTACAGAAAAGCTCCGGACACGA	600
Db	12741	AGAAATGTACTTCTTACATCTGGGGATTTGGAATGTACAGAAAAGCTCCGGACACGA	12800
Qy	601	AGCCCCAGGATGTCCTAAACATGTTCTCAAGTTCCTTACCTGACGTGAGCCCCCAAGCAG	660
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Db	12921	TACTGCTTAGCAGCTCAGCCTCTCAAGAGGAGAGGAGCGAGCTGTGTGATGTGCGTTGA	12980
Qy	781	CTTCTTGGAGGTCGAGCTGAGTGGGAGGGAACATCAATCTCGGGATGGACCCAAA	840
Db	12981	CTTCTTGGAGGTCGAGCTGAGTGGGAGGGAACATCAATCTCGGGATGGACCCAAA	13040

Qy	841	GGAAAGTGGAGGACGTTGTTTCATGTTCTCTGGGCCCCCTAGGCCCTGTTGTTGTTCAAGTC	900
Db	13041	GGAAAGTGGAGGACGTTGTTTCATGTTCTCTGGGCCCCCTAGGCCCTGTTGTTGTTCAAGTC	13100
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Db	13101	AATCATTTCTAGTCTGAGGATTTCAGAGCCCATGTTAATTCATTTGATT	13150
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XX	AC		
XX	AAD37413;		
DT	27-AUG-2002 (first entry)		
XX	Human phospholipase-like enzyme encoding DNA #3.		
DE	Human; phospholipase-like enzyme; cancer; inflammation; Pick's disease;		
KW	cardiovascular disorder; central nervous system disorder; brain injury;		
KW	chronic obstructive pulmonary disease; cerebrovascular disease; dementia;		
KW	Alzheimer's disease; Parkinson's disease; corticobasal degeneration;		
KW	motor neuron disease; Huntington's disease; Creutzfeldt Jacob dementia;		
KW	schizophrenia; Korsakoff's psychosis; pain; epilepsy; multiple sclerosis;		
KW	sciatica; stroke; age associated memory impairment; allergy; asthma;		
KW	allergic rhinitis; hay fever; atopic dermatitis; cardiovascular disease;		
KW	anaphylaxis; inflammation; acute respiratory distress syndrome; diabetes;		
KW	chronic obstructive pulmonary disease; emphysema; obesity; anorexia;		
KW	overweight; cachexia; bulimia; hypertension; coronary artery disease;		
KW	type-II diabetes; hyperlipidaemia; gall bladder disease; osteoarthritis;		
KW	gout; sleep apnoea; respiratory problem; polycystic ovarian syndrome;		
KW	thrombolytic disease; reduced fertility; pregnancy; stress incontinence;		
KW	hirsutism; menstrual irregularity; depression; enzyme; ds.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	WO200231161-A2.		
PN	18-APR-2002.		
XX	09-OCT-2001; 2001WO-EP011641.		
PF	10-OCT-2000; 2000US-0238445P.		
XX	26-DEC-2000; 2000US-0257293P.		
PR	(FARB) BAYER AG.		
XX	Zhu Z;		
PI	WPI; 2002-426287/45.		
XX	New human phospholipase-like enzyme polypeptide useful for screening		
PT	agents, and in the treatment of cancer, inflammation, diabetes, obesity,		
PT	a central nervous system disorder, or a cardiovascular disorder.		
XX	Disclosure; Fig 6; 144pp; English.		
PS	The present invention relates to novel human phospholipase-like enzymes		
XX	and polynucleotides encoding such proteins. Sequences of the invention		
CC	are useful for producing a medicament for modulating the activity of		
CC	phospholipase in a disease such as cancer, inflammation, cardiovascular		
CC	disorders, chronic obstructive pulmonary diseases, central nervous system		
CC	(CNS) disorders such as brain injuries, cerebrovascular disease, dementia		
CC	(Alzheimer's disease), Parkinson's disease, corticobasal degeneration,		
CC	motor neuron disease, Pick's disease, Huntington's disease, Creutzfeld		
CC	Jacob dementia, schizophrenia with dementia, Korsakoff's psychosis, pain		
CC	associated with CNS (e.g. epilepsy, failed back surgery syndrome,		
CC	sciatica), multiple sclerosis, stroke, age associated memory impairment,		
CC	allergic disease including asthma, allergic rhinitis (hay fever), atopic		
CC	dermatitis, anaphylaxis and inflammation, cardiovascular disease, chronic		
CC	obstructive pulmonary disease, acute respiratory distress syndrome, gout,		

Mon Mar 28 09:43:28 2005

us-09-778-961-3_copy_12201_13150.rng

CC diabetes, emphysema or obesity. They are also used for treating anorexia,
CC overweight, cachexia, bulimia, hypertension, type-II diabetes, coronary
CC artery disease, hyperlipidemia, gall bladder disease, osteoarthritis,
CC sleep apnea and respiratory problems, cancer (e.g. breast, prostate,
CC colon cancer), thrombolytic disease, reduced fertility, polycystic
CC ovarian syndrome, complications of pregnancy, menstrual irregularity,
CC hirsutism, stress incontinence and depression. The present sequence is
CC human phospholipase like enzyme encoding DNA

XX Sequence 265 BP; 73 A; 80 C; 62 G; 50 T; 0 U; 0 Other;

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Best Local Similarity 93.8%; Pred. No. 2.4e-11;
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Db 91 TGTCCCACTCAGATGAGCCCTTCTTGAGAACCCCTCGGAATAGTAACTACGTCACCC 150
Qy 427 ATCAAGCCAGCATTTGAG 444
Db 151 ATCAAGCCAGCATTTGAG 168

RESULT 3
AAL01390
ID AAL01390 standard; cDNA; 572 BP.

XX AAL01390;

XX 21-NOV-2001 (first entry)

XX Human reproductive system related antigen cDNA SEQ ID NO: 1391.

XX Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ss.

XX Homo sapiens.

XX WO200155320-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US001339.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 24-FEB-2000; 2000US-0184664P.

XX 02-MAR-2000; 2000US-0186350P.

XX 16-MAR-2000; 2000US-0189874P.

XX 17-MAR-2000; 2000US-0190076P.

XX 18-APR-2000; 2000US-0198123P.

XX 19-MAY-2000; 2000US-0205515P.

XX 07-JUN-2000; 2000US-0209467P.

XX 28-JUN-2000; 2000US-0214886P.

XX 30-JUN-2000; 2000US-0215135P.

XX 07-JUL-2000; 2000US-0216647P.

XX 07-JUL-2000; 2000US-0216880P.

XX 11-JUL-2000; 2000US-0217487P.

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XX 14-JUL-2000; 2000US-0218290P.

XX 26-JUL-2000; 2000US-0220963P.

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XX 14-AUG-2000; 2000US-0224518P.

XX 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225758P.
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PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
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PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
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PR 08-SEP-2000; 2000US-0232080P.
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PR 12-SEP-2000; 2000US-0231968P.
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PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
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PR 21-SEP-2000; 2000US-0234274P.
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PR 25-SEP-2000; 2000US-0234998P.
PR 25-SEP-2000; 2000US-0235484P.
PR 26-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
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PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
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PR 13-OCT-2000; 2000US-0239337P.
PR 13-OCT-2000; 2000US-0239338P.
PR 20-OCT-2000; 2000US-0240560P.
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PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.

14-SEP-2000; 2000US-0233399P.
14-SEP-2000; 2000US-0232400P.
14-SEP-2000; 2000US-0232401P.
14-SEP-2000; 2000US-0233063P.
14-SEP-2000; 2000US-0233064P.
14-SEP-2000; 2000US-0233065P.
14-SEP-2000; 2000US-0234223P.
21-SEP-2000; 2000US-0234274P.
21-SEP-2000; 2000US-0234997P.
25-SEP-2000; 2000US-0234998P.
25-SEP-2000; 2000US-0235484P.
26-SEP-2000; 2000US-0235834P.
27-SEP-2000; 2000US-0235836P.
29-SEP-2000; 2000US-0236327P.
29-SEP-2000; 2000US-0236367P.
29-SEP-2000; 2000US-0236368P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236370P.
02-OCT-2000; 2000US-0236802P.
02-OCT-2000; 2000US-0237037P.
02-OCT-2000; 2000US-0237038P.
02-OCT-2000; 2000US-0237039P.
02-OCT-2000; 2000US-0237040P.
13-OCT-2000; 2000US-0239935P.
13-OCT-2000; 2000US-0239937P.
20-OCT-2000; 2000US-0240960P.
20-OCT-2000; 2000US-0241221P.
20-OCT-2000; 2000US-0241785P.
20-OCT-2000; 2000US-0241786P.
20-OCT-2000; 2000US-0241787P.
20-OCT-2000; 2000US-0241808P.
20-OCT-2000; 2000US-0241809P.
20-OCT-2000; 2000US-0241826P.
01-NOV-2000; 2000US-024617P.
08-NOV-2000; 2000US-0246474P.
08-NOV-2000; 2000US-0246475P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246478P.
08-NOV-2000; 2000US-0246523P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0246525P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246527P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246532P.
08-NOV-2000; 2000US-0246533P.
08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246611P.
08-NOV-2000; 2000US-0246613P.
17-NOV-2000; 2000US-0249207P.
17-NOV-2000; 2000US-0249208P.
17-NOV-2000; 2000US-0249209P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249212P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249215P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249217P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249245P.
17-NOV-2000; 2000US-0249246P.
17-NOV-2000; 2000US-0249247P.
17-NOV-2000; 2000US-0249255P.
17-NOV-2000; 2000US-0249257P.
17-NOV-2000; 2000US-0249259P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0250160P.
01-DEC-2000; 2000US-0250391P.
05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-0251988P.
05-DEC-2000; 2000US-0256719P.
06-DEC-2000; 2000US-0251479P.
08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251858P.
08-DEC-2000; 2000US-0251866P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2000US-0259678P.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-483322/52.
Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.
Claim 1; SEQ ID NO 511; 766pp; English.
The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a cDNA of the invention
XX Sequence 572 BP; 146 A; 159 C; 157 G; 106 T; 0 U; 4 Other;
SQ
Query Match 7.4%; Score 70; DB 4; Length 572;
Best Local Similarity 93.6%; Pred. No. 3.7e-11;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 367 TTTTCTCTTAGAATGAGCCCTTCTCGAGAACCCCTCGGAATAGTACTACGTTACCCC 426
DB 91 TGTCCACTCGAATGAGCCCTTCTCGAGAACCCCTCGGAATAGTACTACGTTACCCC 150
QY 427 ATCAAGCCAGCCATTGAG 444
DB 151 ATCAAGCCAGCCATTGAG 168
RESULT 5
AAH99765
ID AAH99765 standard; cDNA; 802 BP.
XX AAH99765;
AC AAH99765;
XX 16-OCT-2001 (first entry)
DE Human protein encoding cDNA sequence SEQ ID NO:600.
XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
XX anti-inflammatory; antirheumatic; antiarthritic; immunosuppressive;
XX antibacterial; endocrine; cardiac; central nervous system; viricide;
XX anti-HIV; fungicide; antimutagen; cardiovascular; antianemic; anaemia;
XX dermatological; haemostatic; vulnery; antiulcer; osteopathic; eczema;
XX immunoprotective; antiallergic; antiasthmatic; antidiabetic; cytostatic;
XX neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
XX antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
XX cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
XX genetic disease; haematopoietic disorder; platelet disorder; asthma;
XX thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
XX allergic rhinitis; diabetes; multiple sclerosis; depression;
XX Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
XX neuroleptic disorder; ss.
OS Homo sapiens.
XX
PN WO200153455-A2.
PR

XX PD 26-JUL-2001.
 XX PF 22-DEC-2000; 2000WO-US035017.
 XX PR 23-DEC-1999; 99US-00471275.
 XX PR 21-JAN-2000; 2000US-00488725.
 XX PR 23-APR-2000; 2000US-00552317.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Drmanac RT;
 XX PF WPI; 2001-457603/49.
 XX DR P-PSDB; AAM25824.
 XX PT Isolated human polynucleotides encoding polypeptides, useful for the
 XX PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
 XX PS Claim 1; Page 634; 1217pp; English.
 XX CC AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
 XX CC AAM25963. The proteins can have activities based on the tissues and cells
 XX CC they are expressed in, such as: antiinflammatory; antirheumatic;
 XX CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
 XX CC central nervous system; viricide; anti-HIV; fungicide; antimutagen;
 XX CC cardiovascular; anti-nausea; antiaggregant; haemostatic; vulnery;
 XX CC antidiabetic; cytostatic; dermatological; antiallergic; antiasthmatic;
 XX CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
 XX CC encoding them can be used in gene therapy, antisense therapy and vaccine
 XX CC production. The proteins and polynucleotides are useful for screening for
 XX CC agonists or antagonists of a protein and for the treatment and diagnosis
 XX CC of disorders associated with the activity of a protein e.g. inflammation,
 XX CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
 XX CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
 XX CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
 XX CC osteoporosis, severe combined immunodeficiency, eczema, allergic
 XX CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
 XX CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
 XX CC neurological disorders
 XX SQ Sequence 802 BP; 206 A; 236 C; 211 G; 149 T; 0 U; 0 Other;
 Query Match 7.4%; Score 70; DB 4; Length 802;
 Best Local Similarity 93.6%; Pred. No. 4.5e-11;
 Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 367 TTTTCTTTAGATGAGCCCTTCTCGAAGACCCCTCGGAATAGTAACGATACCC 426
 Db 195 TGTCCCACTCAGAATGAGCCCTTCTCGAAGACCCCTCGGAATAGTAACGATACCC 254
 QY 427 ATCAAGCCACCCATTGAG 444
 Db 255 ATCAAGCCACCCATTGAG 272
 RESULT 6
 ABA08297
 ID ABA08297 standard; cDNA; 802 BP.
 XX AC ABA08297;
 XX DT 11-JAN-2002 (first entry)
 XX DE Human phospholipase B homologue-encoding cDNA, SEQ ID NO:73.
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteopathic; vasotropic; cardiant; viricide; antibacterial;
 KW antifungal; vulnery; antiulcer; ss.
 XX OS Homo sapiens.
 XX PN WO200157188-A2.
 XX PD 09-AUG-2001.
 XX PF 05-FEB-2001; 2001WO-US003800.
 XX PR 03-FEB-2000; 2000US-00496914.
 XX PR 27-APR-2000; 2000US-00560875.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Drmanac RT;
 XX PF WPI; 2001-457740/49.
 XX DR P-PSDB; ABB11053.
 XX PT Human proteins and DNA encoding sequences useful for preventing, treating
 XX PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 XX PT and cancer.
 XX PS Claim 1; Page 365; 1963pp; English.
 XX CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 XX CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 XX CC invention also relates to vectors and recombinant host cells comprising a
 XX CC nucleotide of the invention, methods of producing the novel polypeptides,
 XX CC antibodies against the polypeptides, methods of detecting the nucleotides,
 XX CC or polypeptides in a sample, and methods of identifying compounds which
 XX CC bind to polypeptides of the invention. Although novel, many of the
 XX CC polypeptides of the invention have homology to known proteins, thereby
 XX CC giving an insight into their probable biological activities, and hence
 XX CC potential therapeutic applications. The polypeptides of the invention may
 XX CC have various activities, including cytokine, cell proliferation or cell
 XX CC differentiation activities; stem cell growth factor activity;
 XX CC haematopoiesis regulatory activity; tissue growth activity;
 XX CC immunomodulatory activity; activin- or inhibin-related activities;
 XX CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 XX CC thrombolytic activities; receptor or ligand activities; or may be
 XX CC involved in oncogenesis, cancer cell proliferation or metastasis.
 XX CC Depending on their biological activities, polypeptides and nucleotides of
 XX CC the invention are useful for preventing, treating or ameliorating medical
 XX CC conditions, e.g., by protein or gene therapy. Such conditions include
 XX CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 XX CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 XX CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 XX CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 XX CC vascular growth. Polypeptides involved with tissue regeneration and
 XX CC repair (or nucleic acids encoding them) may be used to promote wound
 XX CC healing (e.g., of burns, incisions and ulcers), while those with
 XX CC immunomodulatory activities may be used in the treatment of viral,
 XX CC bacterial and fungal infections in addition to immune disorders.
 XX CC Polypeptides with growth factor activity may be used in cell cultures to
 XX CC promote cell growth. For example, such polypeptides may be used to
 XX CC manipulate stem cells in culture to give rise to neuroepithelial cells
 XX CC that can be used to augment or replace cells damaged by illness,
 XX CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 XX CC may also be used in the diagnosis of the above conditions, and in drug
 XX CC screening techniques. The present sequence represents a cDNA encoding a
 XX CC novel human polypeptide of the invention
 XX SQ Sequence 802 BP; 206 A; 236 C; 211 G; 149 T; 0 U; 0 Other;

us-09-778-961-3_copy_12201_13150.rng

Mon Mar 28 09:43:28 2005

Query Match 7.4%; Score 70; DB 4; Length 802;
Best Local Similarity 93.6%; Pred. NO. 4.5e-11;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 367 TTTTCTCTTGAAGTACGACCCCTCTGAGAACCCCTCGGAATAGTAAGTACACGTACCC 426
195 TGTCCCACTCAGAAATGAGCCCTCTGAGAACCCCTCGGAATAGTAAGTACACGTACCC 254
DB 427 ATCAAGCCAGCCATTGAG 444
255 ATCAAGCCAGCCATTGAG 272
DB
RESULT 7
ABQ82234
ID ABQ82234 standard; cDNA; 1835 BP.
AC ABQ82234;
XX
XX 16-DEC-2002 (first entry)
XX Human phospholipase protein encoding cDNA SEQ ID NO:1.
XX Human; phospholipase; enzyme; chromosome 2; gene; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX 5'UTR 1..175
XX CDS 176..1594
XX /*tag= a
XX /*tag= b
XX /*tag= c
XX 3'UTR 1595..1835
XX /*tag= c
XX WO200262977-A2.
XX PN
XX 15-AUG-2002.
XX PD
XX 28-JAN-2002; 2002WO-US002302.
XX PF
XX 08-FEB-2001; 2001US-00778961.
XX PR (PEKE) PE CORP NY.
XX PA Yan C, Ketchum KA, Di Francesco V, Beasley EM;
XX PI WPI; 2002-692698/73.
XX DR P-PSDB; ABP53556.
XX DR
XX New human phospholipase proteins, useful for the development of human
XX therapeutics and diagnostic compositions, drug screening assays, tissue
XX typing and pharmacogenomic analysis.
XX PS Claim 4; Fig 1A; 95pp; English.
XX
XX The present sequence encodes a human phospholipase protein (I) located on
XX chromosome 2. (I) can be used for identifying agents that modulate its
XX function or activity where the agent is useful for treating a disease or
XX condition mediated by a the human phospholipase protein. (I) peptides can
XX be used in substantial and specific assays related to functional
XX information of the peptide sequences, to raise antibodies or to elicit
XX immune response, as reagents in assays that determine the levels of
XX protein in biological fluids, and as markers for tissues where the
XX corresponding protein is expressed. Nucleotide sequences encoding (I) can
XX be used as probes, primers and chemical intermediates in biological
XX assays, for constructing recombinant vectors, and expressing antigenic
XX portions of the protein. (I) and nucleic acid molecules encoding it can
XX be used in the identification of therapeutic proteins and may serve as
XX models or targets for the development of human therapeutic agents that
XX modulate phospholipase activity in cells and tissues that express the
XX phospholipase, such as in kidney, blood, lung, brain glioblastomas,

CC prostate, colon or leukocytes
XX Sequence 1835 BP; 458 A; 549 C; 474 G; 354 T; 0 U; 0 Other;
SQ
Query Match 7.4%; Score 70; DB 6; Length 1835;
Best Local Similarity 93.6%; Pred. NO. 7.1e-11;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 367 TTTTCTCTTGAAGTACGACCCCTCTGAGAACCCCTCGGAATAGTAAGTACACGTACCC 426
335 TGTCCCACTCAGAAATGAGCCCTCTGAGAACCCCTCGGAATAGTAAGTACACGTACCC 394
DB 427 ATCAAGCCAGCCATTGAG 444
395 ATCAAGCCAGCCATTGAG 412
DB
RESULT 8
AAD37410
ID AAD37410 standard; cDNA; 3648 BP.
AC AAD37410;
XX
XX 27-AUG-2002 (first entry)
XX Human phospholipase-like enzyme encoding cDNA.
XX Human; phospholipase-like enzyme; cancer; inflammation; Pick's disease;
XX cardiovascular disorder; central nervous system disorder; brain injury;
XX chronic obstructive pulmonary disease; cerebrovascular disease; dementia;
XX Alzheimer's disease; Parkinson's disease; corticobasal degeneration;
XX motor neuron disease; Huntington's disease; Creutzfeldt Jacob dementia;
XX schizophrenia; Korsakoff's psychosis; pain; epilepsy; multiple sclerosis;
XX sciatica; stroke; age associated memory impairment; allergy; asthma;
XX allergic rhinitis; hay fever; atopic dermatitis; cardiovascular disease;
XX anaphylaxis; inflammation; acute respiratory distress syndrome; diabetes;
XX chronic obstructive pulmonary disease; emphysema; obesity; anorexia;
XX overweight; cachexia; bulimia; hypertension; coronary artery disease;
XX type-II diabetes; hyperlipidaemia; gall bladder disease; osteoarthritis;
XX gout; sleep apnoea; respiratory problem; polycystic ovarian syndrome;
XX thrombolytic disease; reduced fertility; pregnancy; stress incontinence;
XX hirsutism; menstrual irregularity; depression; enzyme; gene; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 1..3648
XX /*tag= a
XX /*product= "Human phospholipase-like enzyme"
XX /*note= "CDS does not include start and stop codon"
XX /*partial
XX WO200231161-A2.
XX PN
XX 18-APR-2002.
XX PD
XX 09-OCT-2001; 2001WO-EP011641.
XX PF
XX 10-OCT-2000; 2000US-0238445P.
XX PR 26-DEC-2000; 2000US-0257293P.
XX PA (PARB) BAYER AG.
XX XX
XX Zhu Z;
XX WPI; 2002-426287/45.
XX P-PSDB; RAE22860.
XX DR
XX New human phospholipase-like enzyme polypeptide useful for screening
XX agents, and in the treatment of cancer, inflammation, diabetes, obesity,
XX a central nervous system disorder, or a cardiovascular disorder.
XX Claim 19; Fig 1; 144pp; English.
XX PS

XX The present invention relates to novel human phospholipase-like enzymes
 CC and polynucleotides encoding such proteins. Sequences of the invention
 CC are useful for producing a medicament for modulating the activity of
 CC phospholipase in a disease such as cancer, inflammation, cardiovascular
 CC disorders, chronic obstructive pulmonary diseases, central nervous system
 CC (CNS) disorders such as brain injuries, cerebrovascular disease, dementia
 CC (Alzheimer's disease), Parkinson's disease, corticobasal degeneration,
 CC motor neuron disease, Pick's disease, Huntington's disease, Creutzfeldt
 CC Jacob dementia, schizophrenia with dementia, Korsakoff's psychosis, pain
 CC associated with CNS (e.g. epilepsy, failed back surgery syndrome, pain
 CC sciatica), multiple sclerosis, stroke, age associated memory impairment,
 CC allergic disease including asthma, allergic rhinitis (hay fever), atopic
 CC dermatitis, anaphylaxis and inflammation, cardiovascular disease, chronic
 CC obstructive pulmonary disease, acute respiratory distress syndrome, gout,
 CC diabetes, emphysema or obesity. They are also used for treating anorexia,
 CC overweight, cachexia, bulimia, hypertension, type-II diabetes, coronary
 CC artery disease, hyperlipidaemia, gall bladder disease, osteoarthritis,
 CC sleep apnoea and respiratory problems, cancer (e.g. breast, prostate,
 CC colon cancer), thrombolytic disease, reduced fertility, polycystic
 CC ovarian syndrome, complications of pregnancy, menstrual irregularity,
 CC hirsutism, stress incontinence and depression. The present sequence is
 CC human phospholipase like enzyme encoding cDNA
 XX

SQ Sequence 3648 BP; 899 A; 1032 C; 947 G; 770 T; 0 U; 0 Other;

Query Match 7.4%; Score 70; DB 6; Length 3648;

Best Local Similarity 93.6%; Pred. No. 1e-10;

Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 367 TTTTCTCTTAGATGAGCCCTTCTCGAGAACCCCTCGGAATAGTAACTACACGTACCCC 426

Db 2401 TGTCCCACTCAGATGAGCCCTTCTCGAGAACCCCTCGGAATAGTAACTACACGTACCCC 2460

Qy 427 ATCAAGCCAGCATTGAG 444

Db 2461 ATCAAGCCAGCATTGAG 2478

RESULT 9

ID ABX97048 standard; cDNA; 4268 BP.

AC ABX97048;

XX 20-MAY-2003 (first entry)

DT Human NOV24a cDNA.

XX NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;

KW hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;

KW human; gene; ss.

XX Homo sapiens.

OS WO200272757-A2.

XX 19-SEP-2002.

XX 08-MAR-2002; 2002WO-US006908.

XX 08-MAR-2001; 2001US-0274101P.

PR 08-MAR-2001; 2001US-0274194P.

PR 08-MAR-2001; 2001US-0274281P.

PR 08-MAR-2001; 2001US-0274322P.

PR 09-MAR-2001; 2001US-0274849P.

PR 12-MAR-2001; 2001US-0275235P.

PR 13-MAR-2001; 2001US-0275578P.

PR 13-MAR-2001; 2001US-0275579P.

PR 13-MAR-2001; 2001US-0275601P.

PR 14-MAR-2001; 2001US-0276000P.

PR 16-MAR-2001; 2001US-0276766P.

PR 19-MAR-2001; 2001US-0276994P.

PR 20-MAR-2001; 2001US-0277239P.
 PR 20-MAR-2001; 2001US-0277321P.
 PR 20-MAR-2001; 2001US-0277377P.
 PR 21-MAR-2001; 2001US-0277791P.
 PR 22-MAR-2001; 2001US-0277833P.
 PR 23-MAR-2001; 2001US-0278152P.
 PR 26-MAR-2001; 2001US-0278894P.
 PR 27-MAR-2001; 2001US-0278999P.
 PR 27-MAR-2001; 2001US-0279036P.
 PR 28-MAR-2001; 2001US-0279344P.
 PR 30-MAR-2001; 2001US-0279338P.
 PR 30-MAR-2001; 2001US-0279955P.
 PR 30-MAR-2001; 2001US-0280233P.
 PR 02-APR-2001; 2001US-0280802P.
 PR 02-APR-2001; 2001US-0280822P.
 PR 02-APR-2001; 2001US-0280900P.
 PR 04-APR-2001; 2001US-0281194P.
 PR 13-APR-2001; 2001US-0283675P.
 PR 30-APR-2001; 2001US-0287424P.
 PR 02-MAY-2001; 2001US-0288066P.
 PR 03-MAY-2001; 2001US-0288342P.
 PR 03-MAY-2001; 2001US-0288528P.
 PR 15-MAY-2001; 2001US-0291190P.
 PR 16-MAY-2001; 2001US-0291099P.
 PR 16-MAY-2001; 2001US-0291240P.
 PR 30-MAY-2001; 2001US-0294485P.
 PR 31-MAY-2001; 2001US-0294889P.
 PR 31-MAY-2001; 2001US-0294899P.
 PR 18-JUN-2001; 2001US-0299027P.
 PR 19-JUN-2001; 2001US-0299303P.
 PR 19-JUN-2001; 2001US-0299310P.
 PR 10-JUL-2001; 2001US-0304354P.
 PR 13-JUL-2001; 2001US-0309198P.
 PR 16-AUG-2001; 2001US-0312903P.
 PR 10-SEP-2001; 2001US-0318462P.
 PR 12-SEP-2001; 2001US-0318770P.
 PR 27-SEP-2001; 2001US-0325430P.
 PR 27-SEP-2001; 2001US-0325681P.
 PR 18-OCT-2001; 2001US-0330380P.
 PR 31-OCT-2001; 2001US-0335301P.
 PR 14-NOV-2001; 2001US-0332172P.
 PR 14-NOV-2001; 2001US-0332271P.
 PR 14-NOV-2001; 2001US-0332272P.
 PR 14-NOV-2001; 2001US-0333184P.
 PR 21-NOV-2001; 2001US-0333272P.
 PR 03-DEC-2001; 2001US-0332094P.
 PR 03-DEC-2001; 2001US-0337426P.
 PR 04-DEC-2001; 2001US-0338092P.
 PR 03-JAN-2002; 2001US-0337185P.
 PR 07-MAR-2002; 2002US-0045705P.
 PR 07-MAR-2002; 2002US-00092900.

(CURA-) CURAGEN CORP.

Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L;

Zerhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;

Patturajan M, Gangolli E, Vernet CAM, Guo X, Tchernev V;

Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;

Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobrook JP;

Lepley DW, Rieger DK;

WPI; 2002-723332/78.

P-PSDB; ABU65081.

NOVX polypeptides and polynucleotides, useful for preventing or treating

a disorder associated with aberrant NOVX expression or activity e.g.,

cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial

asthma.

Claim 13; Page 167-168; 1103pp; English.

This invention describes novel human NOVX polypeptides which have

cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive

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CC activity. Pharmaceutical compositions comprising the NOVX proteins or
 CC nucleic acid molecules or NOVX antibodies are useful for preventing or
 CC treating a disorder associated with aberrant NOVX expression or activity
 CC e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
 CC asthma. The products of the invention can be used for gene therapy or in
 CC a vaccine. ABX97008-ABX97185 are cDNA fragments amplified and isolated by
 CC the PCR primers and probes represented in ABX13460-ABX13462 and ABX97186-
 CC ABX97593. ABX97008-ABX97185 encode the NOVX proteins described in
 CC ABU65041-ABU65218
 XX Sequence 4268 BP; 1039 A; 1209 C; 1119 G; 901 T; 0 U; 0 Other;
 SQ
 Query Match 7.4%; Score 70; DB 6; Length 4268;
 Best Local Similarity 93.6%; Pred. No. 1.1e-10;
 Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Oy 367 TTTTCTCTTAGAATGAGCCCTTCTCGAGAACCCCTCGAATAGTAACTACAGTACCCC 426
 Db 3016 TGTCCCACTCAGATGAGCCCTTCTCGAGAACCCCTCGAATAGTAACTACAGTACCCC 3075
 Oy 427 ATCAAGCCAGCCATTGAG 444
 Db 3076 ATCAAGCCAGCCATTGAG 3093
 RESULT 10
 ADH42426
 ID ADH42426 standard; DNA; 4268 BP.
 XX
 AC ADH42426;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Novel human nucleic acid NOV65b.
 KW ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic;
 KW anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective;
 KW neurotic; antiparkinsonian; antihypertensive; antinfertility;
 KW cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes;
 KW AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease;
 KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;
 KW tissue typing; preventive medicine; pharmacogenomic; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO2003102159-A2.
 XX
 PD 11-DEC-2003.
 XX
 PF 04-JUN-2003; 2003WO-US017573.
 XX
 PR 04-JUN-2002; 2002US-0385490P.
 PR 04-JUN-2002; 2002US-0385615P.
 PR 04-JUN-2002; 2002US-0385755P.
 PR 05-JUN-2002; 2002US-0386041P.
 PR 06-JUN-2002; 2002US-0386355P.
 PR 06-JUN-2002; 2002US-0386357P.
 PR 06-JUN-2002; 2002US-0386447P.
 PR 06-JUN-2002; 2002US-0386459P.
 PR 06-JUN-2002; 2002US-0386465P.
 PR 06-JUN-2002; 2002US-0386701P.
 PR 07-JUN-2002; 2002US-0386796P.
 PR 07-JUN-2002; 2002US-0386931P.
 PR 07-JUN-2002; 2002US-0387078P.
 PR 07-JUN-2002; 2002US-0387081P.
 PR 10-JUN-2002; 2002US-0387083P.
 PR 10-JUN-2002; 2002US-0387429P.
 PR 10-JUN-2002; 2002US-0387540P.
 PR 10-JUN-2002; 2002US-0387662P.
 PR 11-JUN-2002; 2002US-0387606P.
 PR 11-JUN-2002; 2002US-0387610P.
 PR 11-JUN-2002; 2002US-0387659P.
 PR 11-JUN-2002; 2002US-0387668P.
 PR 11-JUN-2002; 2002US-0387698P.
 PR 11-JUN-2002; 2002US-0387934P.
 PR 12-JUN-2002; 2002US-0387960P.
 PR 12-JUN-2002; 2002US-0388022P.
 PR 12-JUN-2002; 2002US-0388096P.
 PR 12-JUN-2002; 2002US-0388432P.
 PR 12-JUN-2002; 2002US-0388479P.
 PR 12-JUN-2002; 2002US-0389123P.
 PR 13-JUN-2002; 2002US-0389120P.
 PR 14-JUN-2002; 2002US-0389146P.
 PR 17-JUN-2002; 2002US-0389742P.
 PR 18-JUN-2002; 2002US-0389604P.
 PR 18-JUN-2002; 2002US-0389884P.
 PR 19-JUN-2002; 2002US-0390006P.
 PR 19-JUN-2002; 2002US-0390144P.
 PR 19-JUN-2002; 2002US-0390209P.
 PR 25-JUN-2002; 2002US-0391726P.
 PR 06-AUG-2002; 2002US-0401628P.
 PR 09-AUG-2002; 2002US-0402268P.
 PR 12-AUG-2002; 2002US-0402822P.
 PR 13-AUG-2002; 2002US-0403458P.
 PR 15-AUG-2002; 2002US-0403617P.
 PR 15-AUG-2002; 2002US-0403732P.
 PR 26-AUG-2002; 2002US-0406182P.
 PR 12-SEP-2002; 2002US-0410085P.
 PR 13-SEP-2002; 2002US-0410505P.
 PR 23-SEP-2002; 2002US-0412955P.
 PR 30-SEP-2002; 2002US-0415195P.
 PR 23-OCT-2002; 2002US-0420627P.
 PR 23-OCT-2002; 2002US-0420718P.
 PR 24-OCT-2002; 2002US-0420852P.
 PR 31-OCT-2002; 2002US-0422750P.
 PR 01-NOV-2002; 2002US-0423095P.
 PR 05-NOV-2002; 2002US-0423748P.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 PA Albrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;
 PI Burgess CE, Casman SJ, Catterton E, Dhanabai M, Edinger SR;
 PI Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
 PI Grosche WM, Gunther B, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda R;
 PI Khrantsov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR;
 PI MacLachlan T, Malyankar UM, McQueeney K, Mezick AJ, Miller CE;
 PI Millet I, Padigaru M, Patturajan M, Peyman JA, Qian X, Rastelli L;
 PI Rieger DK, Rothenberg ME, Shenoy SG, Shinkets RA, Smithson G;
 PI Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CM, Voss EZ;
 PI Wolenc AR, Zhong M, Zhong H;
 XX
 XX WPI; 2004-053467/05.
 DR P-PSDB; ADH42427.
 DR
 XX
 XX New NOVX polypeptides and nucleic acid molecules useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
 PT atherosclerosis or diabetes, in chromosome mapping, tissue typing or in
 PT pharmacogenomics.
 XX
 XX Claim 20; SEQ ID NO 979; 1503pp; English.
 PS
 XX The invention relates to 566 new isolated human polypeptides and their
 CC encoding genes, sequences that are at least 95% identical to these or
 CC sequences comprising one or more conservative substitutions in these. The
 CC polypeptide, polynucleotide and antibodies against the polypeptides are
 CC useful in diagnosing, treating or preventing NOVX-associated disorders,
 CC e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
 CC diabetes, AIDS, multiple sclerosis, graft-versus-host disease,
 CC Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.
 CC The nucleic acids are further used as hybridization probes, in chromosome
 CC mapping, tissue typing, preventive medicine, and pharmacogenomics. The
 CC polypeptides are also useful as vaccines. This sequence represents an
 CC example of the nucleic acid sequence of the invention.
 XX

SQ Sequence 4268 BP; 1039 A; 1209 C; 1119 G; 901 T; 0 U; 0 Other;

Query Match 7.4%; Score 70; DB 12; Length 4268;

Best Local Similarity 93.6%; Pred. No. 1.1e-10;

Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 367 TTTTCTCTTGAATGAGCCCTTCTGAGAACCCCTCGGAATAGTAACACGTACCCC 426

Db 3016 TGTCCCACTCAGATGAGCCCTTCTGAGAACCCCTCGGAATAGTAACACGTACCCC 3075

Qy 427 ATCAAGCCAGCCATTGAG 444

Db 3076 ATCAAGCCAGCCATTGAG 3093

RESULT 11

ADN61812

ID ADN61812 standard; cDNA; 4268 BP.

XX AC ADN61812;

XX DT 01-JUL-2004 (first entry)

XX DE Human cDNA encoding NOV24a.

XX KW Human; ss; gene; NOVX; diabetes; obesity; infectious disease; anorexia;

KW cancer-associated cachexia; cancer; neurodegenerative disorder;

KW Alzheimer's disease; Parkinson's disease; immune disorder;

KW haematopoietic disorder; dyslipidaemia; chronic disease.

XX OS Homo sapiens.

XX PN US2004043382-A1.

XX PD 04-MAR-2004.

XX PF 07-MAR-2002; 2002US-00092300.

XX 08-MAR-2001; 2001US-0274191P.

PR 08-MAR-2001; 2001US-0274194P.

PR 08-MAR-2001; 2001US-0274281P.

PR 08-MAR-2001; 2001US-0274322P.

PR 09-MAR-2001; 2001US-0274849P.

PR 12-MAR-2001; 2001US-0275235P.

PR 13-MAR-2001; 2001US-0275578P.

PR 13-MAR-2001; 2001US-0275579P.

PR 13-MAR-2001; 2001US-0275601P.

PR 14-MAR-2001; 2001US-0276000P.

PR 16-MAR-2001; 2001US-0276776P.

PR 19-MAR-2001; 2001US-0276994P.

PR 20-MAR-2001; 2001US-0277239P.

PR 20-MAR-2001; 2001US-0277321P.

PR 20-MAR-2001; 2001US-0277327P.

PR 20-MAR-2001; 2001US-0277338P.

PR 21-MAR-2001; 2001US-0277791P.

PR 22-MAR-2001; 2001US-0277833P.

PR 23-MAR-2001; 2001US-0278152P.

PR 26-MAR-2001; 2001US-0278894P.

PR 27-MAR-2001; 2001US-0278998P.

PR 27-MAR-2001; 2001US-0279036P.

PR 28-MAR-2001; 2001US-0279344P.

PR 30-MAR-2001; 2001US-0279995P.

PR 30-MAR-2001; 2001US-0280233P.

PR 02-APR-2001; 2001US-0280802P.

PR 02-APR-2001; 2001US-0280822P.

PR 02-APR-2001; 2001US-0280900P.

PR 04-APR-2001; 2001US-0281444P.

PR 13-APR-2001; 2001US-0283675P.

PR 30-APR-2001; 2001US-0287424P.

PR 02-MAY-2001; 2001US-0288066P.

PR 03-MAY-2001; 2001US-0288342P.

PR 03-MAY-2001; 2001US-0288528P.

PR 15-MAY-2001; 2001US-0291190P.

PR 16-MAY-2001; 2001US-0291099P.

PR 16-MAY-2001; 2001US-0291240P.

PR 30-MAY-2001; 2001US-0294485P.

PR 31-MAY-2001; 2001US-0294889P.

PR 31-MAY-2001; 2001US-0294899P.

PR 18-JUN-2001; 2001US-0299027P.

PR 19-JUN-2001; 2001US-0299303P.

PR 19-JUN-2001; 2001US-0299310P.

PR 10-JUL-2001; 2001US-0304354P.

PR 31-JUL-2001; 2001US-0309198P.

PR 16-AUG-2001; 2001US-0312903P.

PR 10-SEP-2001; 2001US-0318462P.

PR 12-SEP-2001; 2001US-0318770P.

PR 27-SEP-2001; 2001US-0325430P.

PR 27-SEP-2001; 2001US-0325681P.

PR 18-OCT-2001; 2001US-0330380P.

PR 31-OCT-2001; 2001US-0335301P.

PR 14-NOV-2001; 2001US-0332172P.

PR 14-NOV-2001; 2001US-0332271P.

PR 14-NOV-2001; 2001US-0332272P.

PR 14-NOV-2001; 2001US-0333184P.

PR 21-NOV-2001; 2001US-0332722P.

PR 21-NOV-2001; 2001US-0332094P.

PR 03-DEC-2001; 2001US-0337426P.

PR 03-DEC-2001; 2001US-0338092P.

PR 04-DEC-2001; 2001US-0337185P.

PR 03-JAN-2002; 2002US-0345705P.

XX (PADI/) PADIGARU M.

PA (SPYT/) SPYTEK K A.

PA (SHEN/) SHENOY S G.

PA (TAUP/) TAUPIER R J.

PA (PENA/) PENA C E A.

PA (LILL/) LI L.

PA (ZERH/) ZERHUSEN B D.

PA (GUSE/) GUSEV V Y.

PA (JIWV/) JI W.

PA (GORM/) GORMAN L.

PA (MILL/) MILLER C E.

PA (KEKU/) KEKUDA R.

PA (PATT/) PATTURAJAN M.

PA (GANG/) GANGOLLI E A.

PA (VERN/) VERNET C A M.

PA (GUOX/) GUO X S.

PA (TCHE/) TCHERNEV V T.

PA (FERN/) FERNANDES E R.

PA (CASM/) CASMAN S J.

PA (MALY/) MALYANKAR U M.

PA (GERL/) GERLACH V.

PA (LIUY/) LIU Y.

PA (ANDE/) ANDERSON D W.

PA (SPAD/) SPADERNA S K.

PA (CATT/) CATTERTON E.

PA (LEIT/) LEITE M W.

PA (ZHON/) ZHONG H.

PA (ALSO/) ALSOBROOK J P.

PA (LEPL/) LEPLEY D M.

PA (RIEG/) RIEGER D K.

PA (BURG/) BURGESS C E.

XX Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CE, Li L;

PI Zerkhusen BD, Gusev VY, Ji W, Gorman L, Miller CE, Kekuda R;

PI Patturajan M, Gangolli EA, Vernet CAM, Guo XS, Tchernev VT;

PI Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y;

PI Anderson DW, Spaderna SK, Catterton E, Leite MW, Zhong H;

PI Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;

XX WPI; 2004-225693/21.

DR P-PSDB; ADN61813.

XX New NOVX polypeptides and nucleic acid molecules useful for diagnosing,

PT preventing or treating NOVX-associated disorders, e.g. cancer, diabetes,

PT infection or obesity, and in chromosome mapping, tissue typing or

XX PA (INCY-) INCYTE CORP.

XX PI Khare R, Kable AE, Lee SY, Hafalia AJA, Chawla NK, Marquis JP;

XX PI Ramkumar J, Wilson AD, Jin P, Hawkins PR, Bulloch SA, Swarnakar A;

XX PI Elliott VS, Richardson TW, Mason PM, Baughn MR, Yue H, Becha SD;

XX PI Tang YT, Batra S, Lu DAM, Bhatia UG, Burrill JD, Lee S, Blake JJ;

XX PI Ho A, Zheng W, Gao J;

XX WPI; 2004-053042/05.

DR P-PSDB; ADH13664.

DR

XX New human enzymes (ENZM), useful for diagnosing, treating and preventing

XX diseases or conditions associated with the aberrant ENZM expression e.g.

XX cancer, AIDS, atherosclerosis, epilepsy, or infections.

XX Claim 5; SEQ ID NO 86; 463pp; English.

XX This invention relates to novel human enzymes (ENZM) and the genes which

XX encode them. The invention may be useful for the development of compounds

XX with a cytostatic, antiarteriosclerotic, anticonvulsant, neurotropic,

XX neuroprotective, cerebroprotective, anti-HIV, antiallergic,

XX antiinflammatory or thymimetic activity or for gene therapy. The

XX invention may therefore be useful in diagnosing, treating and preventing

XX diseases or conditions associated with the decreased expression or

XX overexpression of ENZM, such as cell proliferative (for example cancer,

XX atherosclerosis), neurological (for example AIDS, allergies) and

XX disease, stroke), immune/inflammatory (for example Cushing's syndrome) disorders

XX developmental (for example Hypothyroidism, Cushing's syndrome) effects of

XX or infections. These are also useful in assessing the effects of

XX exogenous compounds on the expression of nucleic acid and amino acid

XX sequences of ENZM. The present sequence is that of a gene which encodes a

XX human ENZM enzyme of the invention.

XX Sequence 4311 BP; 1076 A; 1198 C; 1130 G; 907 T; 0 U; 0 Other;

XX SQ

Query Match 7.4%; Score 70; DB 12; Length 4311;

Best Local Similarity 93.6%; Pred. No. 1.1e-10;

Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 367 TTTTCTCTTAGAATGAGCCCTTCTGAGAACCCCTCGGAATAGTACTACAGTACCCC 426

Db 2843 TGTCCCACTCAGATGAGCCCTTCTGAGAACCCCTCGGAATAGTACTACAGTACCCC 2902

QY 427 ATCAAGCCAGCCATTGAG 444

Db 2903 ATCAAGCCAGCCATTGAG 2920

RESULT 13

ABQ77623

ID ABQ77623 standard; cDNA; 4377 BP.

XX AC ABQ77623;

XX DT 21-OCT-2002 (first entry)

XX DE Human lipase NHL (Ala 1318 variant) cDNA.

XX KW Human; lipase; chromosome 2; phospholipase B homologue; thyroid; brain;

XX KW inflammatory disease; proliferative disease; infectious disease;

XX KW clotting disorder; cancer; drug screening; mental disorder; NHL;

XX KW diagnostic reagent; clinical trial monitoring; cosmetic; nutraceutical;

XX KW mutation detection; gene expression analysis; transgenic animal;

XX KW neurotropic; cytostatic; antiinflammatory; single nucleotide polymorphism;

XX KW SNP; gene therapy; gene; ss.

XX OS Homo sapiens.

XX FH Key

XX CDS 1..4377

XX FT /*tag= a

XX FT /product= "Human lipase NHL"

PT pharmacogenomics.

XX Claim 17; SEQ ID NO 81; 786pp; English.

XX The invention relates to an isolated polypeptide (designated NOVX, or

XX NOV1-NOV127) comprising a sequence selected from 178 fully defined amino

XX acid sequences (and their mature forms, variants and fragments). Also

XX included are an isolated nucleic acid molecule encoding NOVX, a vector

XX comprising the nucleic acid, a cell comprising the vector, methods for

XX determining the presence or amount of the polypeptide or the nucleic acid

XX molecule in a sample, methods for determining the presence of or

XX predisposition to a disease associated with altered levels of expression

XX of the above polypeptide or nucleic acid molecule in a first mammalian

XX subject, a method for identifying an agent that binds to the above

XX polypeptide, a method for identifying a potential therapeutic agent for

XX use in the treatment of a pathology that is related to aberrant

XX expression or physiological interactions of the polypeptide, a method of

XX screening for a modulator of activity or of latency or predisposition to

XX a pathology associated with the polypeptide and a method for modulating

XX the activity of the polypeptide cited above. The composition and methods

XX are useful for diagnosing, preventing or treating diseases such as

XX diabetes, obesity, infectious diseases, anorexia, cancer-associated

XX cachexia, cancer, neurodegenerative disorders like Alzheimer's disease or

XX parkinson's disease, immune disorders, haematopoietic disorders,

XX dyslipidaemias, and other chronic diseases. These may also be used in

XX chromosome mapping, tissue typing, preventive medicine and

XX pharmacogenomics. The polypeptides are also useful as vaccines. The

XX present sequence encodes a NOVX protein of the invention.

XX Sequence 4268 BP; 1039 A; 1214 C; 1114 G; 901 T; 0 U; 0 Other;

XX SQ

Query Match 7.4%; Score 70; DB 12; Length 4268;

Best Local Similarity 93.6%; Pred. No. 1.1e-10;

Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 367 TTTTCTCTTAGAATGAGCCCTTCTGAGAACCCCTCGGAATAGTACTACAGTACCCC 426

Db 3016 TGTCCCACTCAGATGAGCCCTTCTGAGAACCCCTCGGAATAGTACTACAGTACCCC 3075

QY 427 ATCAAGCCAGCCATTGAG 444

Db 3076 ATCAAGCCAGCCATTGAG 3093

RESULT 12

ADH13733

ID ADH13733 standard; DNA; 4311 BP.

XX AC ADH13733;

XX DT 11-MAR-2004 (first entry)

XX DE Human ENZM enzyme gene sequence SeqID86.

XX KW human; ENZM; cytostatic; antiarteriosclerotic; anticonvulsant; neurotropic;

XX KW neuroprotective; cerebroprotective; anti-HIV; antiallergic;

XX KW antiinflammatory; thymimetic; gene therapy;

XX KW cell proliferative disorder; cancer; atherosclerosis;

XX KW neurological disorder; epilepsy; Huntington's disease; stroke;

XX KW immune disorder; inflammatory disorder; AIDS; allergy;

XX KW developmental disorder; Hypothyroidism; Cushing's syndrome; infection;

XX KW gene; ds.

XX OS Homo sapiens.

XX PN WO2003093439-A2.

XX PD 13-NOV-2003.

XX PF 29-APR-2003; 2003WO-US013821.

XX PR 29-APR-2002; 2002US-0376506P.

XX PR 17-MAY-2002; 2002US-0381558P.

FT variation replace(3953, T)
FT /*tag= b
FT /note= "Single nucleotide polymorphism (SNP); leads to an
FT Ala to Val substitution at position 1318 of the protein"
XX
PN WO200259328-A1.
PD
PD 01-AUG-2002.
PF 22-JAN-2002; 2002WO-US001715.
PF 24-JAN-2001; 2001US-0264049P.
XX (LEXI-) LEXICON GENETICS INC.
XX Yu X, Miranda M, Turner CA;
XX WPI; 2002-599797/64.
XX P-PSDB; ABB09555.
XX
XX Polynucleotides encoding human lipases that are structurally related to
XX animal lipases, particularly phospholipase B, useful for drug screening,
XX diagnosis and in gene therapy of biological disorders.
XX
XX Claim 1; Page 36-37; 44pp; English.
XX
XX The invention relates to a novel human lipase (NHL; ABB09555, ABB09556)
XX and to nucleic acids encoding it (ABQ77623, ABQ77624). The NHL has
XX structural similarity with animal lipases, particularly phospholipase B.
XX Polynucleotides encoding NHL were obtained using human genomic sequences
XX in conjunction with human thyroid and brain cDNAs. The NHL gene is
XX located on chromosome 2, and contains a C/T polymorphism at position 3953
XX of the open reading frame (ORF), resulting in an Ala/Val substitution at
XX position 1318 in the protein. NHL nucleotides and proteins are useful for
XX treating disorders such as inflammatory or proliferative disease, and
XX infectious diseases, clotting disorders, and cancer. They can also be used
XX in screening for compounds useful in the treatment of mental, biological
XX or medical disorders, as diagnostic reagents, in clinical trial
XX monitoring and in cosmetic and nutraceutical applications. NHL
XX nucleotides can additionally be used in the detection of disease-
XX associated mutations, in the analysis of gene expression, for the
XX recombinant expression of NHL, to generate transgenic animals, in gene
XX therapy, and as part of ribozyme and/or triple helix sequences useful in
XX the modulation of NHL gene expression. The present sequence represents
XX cDNA encoding the Ala 1318 variant of NHL
XX
XX Sequence 4377 BP; 1085 A; 1217 C; 1155 G; 920 T; 0 U; 0 Other;
SQ

Query Match 7.4%; Score 70; DB 6; Length 4377;
Best Local Similarity 93.6%; Pred. No. 1.1e-10;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 367 TTTTCTCTTAGAATGAGCCCTTCTCGAGACCCCTCGGAATAGTAACTACACGTACCCC 426
Db 3118 TGTCCCACTCAGATGAGCCCTTCTCGAGACCCCTCGGAATAGTAACTACACGTACCCC 3177

Qy 427 ATCAAGCCAGCCATTGAG 444
Db 3178 ATCAAGCCAGCCATTGAG 3195

RESULT 14
ABQ77624
ID ABQ77624 standard; cDNA; 4377 BP.
XX
XX AC ABQ77624;
XX
XX 21-OCT-2002 (first entry)
XX
XX Human lipase NHL (Val 1318 variant) cDNA.
XX
XX Human; lipase; chromosome 2; phospholipase B homologue; thyroid; brain;
KW inflammatory disease; proliferative disease; infectious disease;

clotting disorder; cancer; drug screening; mental disorder; NHL;
diagnostic reagent; clinical trial monitoring; cosmetic; nutraceutical;
mutation detection; gene expression analysis; transgenic animal;
nootropic; cytostatic; antiinflammatory; single nucleotide polymorphism;
SNP; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..4377
XX /*tag= a
XX /product= "Human lipase NHL"
XX /replace(3953, C)
XX /tag= b
XX /note= "Single nucleotide polymorphism (SNP); leads to a
XX Val to Ala substitution at position 1318 of the protein"
XX
XX WO200259328-A1.
XX
XX 01-AUG-2002.
XX
XX 22-JAN-2002; 2002WO-US001715.
XX
XX 24-JAN-2001; 2001US-0264049P.
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Yu X, Miranda M, Turner CA;
XX WPI; 2002-599797/64.
XX P-PSDB; ABB09555.
XX
XX Polynucleotides encoding human lipases that are structurally related to
XX animal lipases, particularly phospholipase B, useful for drug screening,
XX diagnosis and in gene therapy of biological disorders.
XX
XX Disclosure; Page; 44pp; English.
XX
XX The invention relates to a novel human lipase (NHL; ABB09555, ABB09556)
XX and to nucleic acids encoding it (ABQ77623, ABQ77624). The NHL has
XX structural similarity with animal lipases, particularly phospholipase B.
XX Polynucleotides encoding NHL were obtained using human genomic sequences
XX in conjunction with human thyroid and brain cDNAs. The NHL gene is
XX located on chromosome 2, and contains a C/T polymorphism at position 3953
XX of the open reading frame (ORF), resulting in an Ala/Val substitution at
XX position 1318 in the protein. NHL nucleotides and proteins are useful for
XX treating disorders such as inflammatory or proliferative disease, and
XX infectious diseases, clotting disorders, and cancer. They can also be used
XX in screening for compounds useful in the treatment of mental, biological
XX or medical disorders, as diagnostic reagents, in clinical trial
XX monitoring and in cosmetic and nutraceutical applications. NHL
XX nucleotides can additionally be used in the detection of disease-
XX associated mutations, in the analysis of gene expression, for the
XX recombinant expression of NHL, to generate transgenic animals, in gene
XX therapy, and as part of ribozyme and/or triple helix sequences useful in
XX the modulation of NHL gene expression. The present sequence represents
XX cDNA encoding the Val 1318 variant of NHL. Note: The present sequence is
XX not shown in the specification, but was derived from the the information
XX given on page 18 and the Ala 1318 NHL-encoding cDNA (ABQ77623) given in
XX the sequence listing
XX
XX Sequence 4377 BP; 1085 A; 1216 C; 1155 G; 921 T; 0 U; 0 Other;
SQ

Query Match 7.4%; Score 70; DB 6; Length 4377;
Best Local Similarity 93.6%; Pred. No. 1.1e-10;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 367 TTTTCTCTTAGAATGAGCCCTTCTCGAGACCCCTCGGAATAGTAACTACACGTACCCC 426
Db 3118 TGTCCCACTCAGATGAGCCCTTCTCGAGACCCCTCGGAATAGTAACTACACGTACCCC 3177

Qy 427 ATCAAGCCAGCCATTGAG 444
Db 3178 ATCAAGCCAGCCATTGAG 444

RESULT 14
ABQ77624
ID ABQ77624 standard; cDNA; 4377 BP.
XX
XX AC ABQ77624;
XX
XX 21-OCT-2002 (first entry)
XX
XX Human lipase NHL (Val 1318 variant) cDNA.
XX
XX Human; lipase; chromosome 2; phospholipase B homologue; thyroid; brain;
KW inflammatory disease; proliferative disease; infectious disease;

XX WPI; 2003-120797/11.
DR P-PSDB; AAE34448.
XX New human lipid-associated molecule (LIPAM) proteins and polynucleotides,
PT useful for diagnosing, treating or preventing cardiovascular disorders
PT (e.g. aneurysms), neurological disorders (e.g. Parkinson's disease) or
PT cancers.
XX Claim 74; Page 168-169; 171pp; English.
XX The present invention relates to novel human lipid-associated molecules
CC (LIPAM) and polynucleotides encoding such proteins. Sequences of the
CC invention are useful for treating diseases or conditions associated with
CC decreased expression of functional LIPAM. The antagonist is useful for
CC treating a disease or condition associated with the overexpression of
CC functional LIPAM. They are useful for diagnosing, treating or preventing
CC cardiovascular disorders (e.g. arteriovenous fistula, atherosclerosis,
CC hypertension, Raynaud's disease, angina pectoris, ischaemic heart disease
CC heart failure, thrombophlebitis, aneurysms, varicose veins, congestive
CC oesophagitis, nausea, peptic ulcer or Crohn's disease), lipid metabolism
CC disorders (e.g. fatty liver, Fabry's disease, Gaucher's disease, diabetes
CC mellitus, hyperlipidaemia, hypercholesterolaemia), autoimmune disorders
CC or inflammatory disorders (e.g. acquired immunodeficiency syndrome,
CC anaemia, asthma or Crohn's disease), neurological disorders (e.g. stroke,
CC epilepsy, dementia, Alzheimer's disease), or prion diseases such as kuru
CC or Creutzfeldt-Jakob disease) or cancers (e.g. adenocarcinoma, leukaemia,
CC lymphoma, melanoma, myeloma or sarcoma). They are also used in gene
CC therapy and protein replacement therapy. The present sequence is human
CC LIPAM-9 cDNA
XX Sequence 4424 BP; 1119 A; 1231 C; 1143 G; 931 T; 0 U; 0 Other;
SQ

XX Query Match 7.4%; Score 70; DB 8; Length 4424;
Best Local Similarity 93.6%; Pred. No. 1.2e-10;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 367 TTTTCTCTTGAATGAGCCCTTCTGTAGAACCCCTCGGATAGTACTACGTACCCC 426
DB 2939 TGTCCCACTCAGATGAGCCCTTCTGTAGAACCCCTCGGATAGTACTACGTACCCC 2998
QY 427 ATCAAGCCAGCCATTGAG 444
DB 2999 ATCAAGCCAGCCATTGAG 3016
Search completed: March 26, 2005, 14:31:27
Job time : 496.725 secs

XX Human, lipid-associated molecule; LIPAM; cardiovascular disorder; stroke;
KW arteriovenous fistula; atherosclerosis; hypertension; Raynaud's disease;
KW aneurysm; congestive heart failure; thrombophlebitis; angina pectoris;
KW ischaemic heart disease; rheumatic heart disease; peptic oesophagitis;
KW gastrointestinal disorder; lipid metabolism disorder; Crohn's disease;
KW nausea; peptic ulcer; fatty liver; Fabry's disease; Gaucher's disease;
KW diabetes mellitus; hyperlipidaemia; hypercholesterolaemia; epilepsy;
KW autoimmune disorder; inflammatory disorder; neurological disorder; kuru;
KW acquired immunodeficiency syndrome; anaemia; Alzheimer's disease; asthma;
KW dementia; prion disease; Creutzfeldt-Jakob disease; leukaemia; cancer;
KW adenocarcinoma; lymphoma; melanoma; myeloma; sarcoma; gene therapy;
KW protein replacement therapy; gene; ss.
XX Homo sapiens.
XX Location/Qualifiers
FH 9..2918
FT /tag= a
FT /product= "Human LIPAM-9 protein"
FT 9..83
FT /tag= h
FT sig_peptide
FT 9..74
FT /tag= f
FT sig_peptide
FT 9..71
FT /tag= d
FT sig_peptide
FT 9..65
FT /tag= b
FT mat_peptide
FT 66..2915
FT /tag= c
FT /product= "Human mature LIPAM-9 protein"
FT 72..2915
FT /tag= e
FT mat_peptide
FT 75..2915
FT /product= "Human mature LIPAM-9 protein"
FT /tag= g
FT mat_peptide
FT 84..2915
FT /product= "Human mature LIPAM-9 protein"
FT /tag= i
FT /product= "Human mature LIPAM-9 protein"
XX WO200294988-A2.
XX 28-NOV-2002.
XX 17-MAY-2002; 2002WO-US015688.
XX 18-MAY-2001; 2001US-0292242P.
XX 25-MAY-2001; 2001US-0293726P.
XX 01-JUN-2001; 2001US-0295346P.
XX 06-JUL-2001; 2001US-0303404P.
XX 24-AUG-2001; 2001US-0314754P.
XX 22-JAN-2002; 2002US-0351262P.
XX 29-MAR-2002; 2002US-0368799P.
XX (INCY-) INCYTE GENOMICS INC.
XX Tang YT, Yue H, Azimzai Y, Baughn MR, Burford N, Reddy R;
PI Wallia NK, Das D, Nguyen DB, Yao MG, Lu Y, Gandhi AR;
PI Griffin JA, Elliott VS, Ramkumar J, Lal PG, Lu DAM, Lee SY;
PI Yue H, Yang J, Tribouley CM, Kable AB, Swarnakar A;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 13:16:45 ; Search time 167.092 Seconds
(without alignments)
9303.061 Million cell updates/sec

Title: US-09-778-961-3_COPY_12201_13150
Perfect score: 950
Sequence: 1 taatcatacaacttcttggg.....atggtaattccattggatt 950

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40.6	4.3	96074	4	US-09-949-016-12760
2	40.6	4.3	96074	4	US-09-949-016-12760
3	39.6	4.1	507	4	US-09-543-681A-2163
4	38.6	4.1	225127	4	US-09-949-016-16480
5	37.8	4.0	285	4	US-09-543-681A-1767
6	37.2	3.9	399	4	US-09-621-976-8976
7	36.2	3.8	451924	4	US-09-949-016-12896
8	36.2	3.8	451925	4	US-09-949-016-17305
9	35.8	3.8	101349	4	US-09-949-016-17433
10	35.6	3.7	160018	4	US-09-949-016-12617
11	35.6	3.7	160018	4	US-09-949-016-15994
12	35.4	3.7	782	3	US-08-998-416-224
13	35.2	3.7	601	4	US-09-949-016-84673
14	35.2	3.7	69764	4	US-09-949-016-15638
15	35.2	3.7	321022	4	US-09-949-016-11852
16	35.2	3.7	321022	4	US-09-949-016-14166
17	34.8	3.7	93532	4	US-09-949-016-15944
18	34.6	3.6	7218	1	US-08-232-463-14
19	34.4	3.6	197875	4	US-09-949-016-15425
20	34.2	3.6	6136	1	US-08-137-252-1
21	34.2	3.6	54945	4	US-09-967-669-10
22	34.2	3.6	65485	4	US-09-949-016-13757
23	34.2	3.6	65552	4	US-09-949-016-12303
24	34.2	3.6	177797	4	US-09-949-016-14125
25	34.2	3.6	227979	4	US-09-949-016-11842
26	34	3.6	1497	4	US-09-107-532A-3423
27	34	3.6	13335	4	US-09-949-016-14676

28	34	3.6	139562	4	US-09-949-016-13451
29	33.8	3.6	601	4	US-09-949-016-166679
30	33.8	3.6	601	4	US-09-949-016-205536
31	33.8	3.6	904	4	US-09-270-767-195
32	33.8	3.6	904	4	US-09-270-767-15477
33	33.8	3.6	96202	4	US-09-949-016-16433
34	33.8	3.6	194933	4	US-09-949-016-14172
35	33.8	3.6	271134	4	US-09-949-016-12705
36	33.8	3.6	305491	4	US-09-949-016-17550
37	33.8	3.6	387902	4	US-09-949-016-14543
38	33.8	3.6	421883	4	US-09-949-016-12557
39	33.6	3.5	19377	4	US-09-949-016-15198
40	33.6	3.5	45484	4	US-09-949-016-12967
41	33.4	3.5	972	4	US-09-891-641-9
42	33.4	3.5	151295	4	US-09-949-016-14568
43	33.4	3.5	151295	4	US-09-949-016-14569
44	33.4	3.5	151295	4	US-09-949-016-14570
45	33.4	3.5	151295	4	US-09-949-016-14571

ALIGNMENTS

RESULT 1

US-09-949-016-12760
; Sequence 12760, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12760
; LENGTH: 96074
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12760

Query Match 4.3%; Score 40.6; DB 4; Length 96074;
Best Local Similarity 55.2%; Pred. No. 0.21;
Matches 79; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
Qy 234 AATTATGTTTATCAGTCTTTCTATATAGTCAGAGAGATCATGTAAATAATCTAC 293
Db 36911 AATTATATTTTAAAGATAATTTTATATAATGCAAAACCTTTTATCATGTACAATCT 36970
Qy 294 AGGCAGGATTGTAGTTTCTCTTCTCTCAAGCAAACTTCAGTGCTGTCAGATAACTTC 353
Db 36971 GGTAAACACCTTGAGTAATTTGTCATTCACATGCACATTTTATTGTTTCATTAATCTTTT 37030
Qy 354 TCAGTGTGTTTTTTTTTCTCTT 376
Db 37031 TCTTTGTTTATTTTTCTGTT 37053

RESULT 2

US-09-949-016-13611
; Sequence 13611, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

Sequence 16480, Application US/09949016						
Patent No. 6812339						
GENERAL INFORMATION:						
APPLICANT: VENTER, J. Craig et al.						
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF						
FILE REFERENCE: CLO01307						
CURRENT APPLICATION NUMBER: US/09/949,016						
CURRENT FILING DATE: 2000-04-14						
PRIOR APPLICATION NUMBER: 60/241,755						
PRIOR FILING DATE: 2000-10-20						
PRIOR APPLICATION NUMBER: 60/237,768						
PRIOR FILING DATE: 2000-10-03						
PRIOR APPLICATION NUMBER: 60/231,498						
PRIOR FILING DATE: 2000-09-08						
NUMBER OF SEQ ID NOS: 207012						
SOFTWARE: FastSeq for Windows Version 4.0						
SEQ ID NO 16480						
LENGTH: 225127						
TYPE: DNA						
ORGANISM: Human						
FEATURE:						
NAME/KEY: misc feature						
LOCATION: (1)...(225127)						
OTHER INFORMATION: n = A,T,C or G						
US-09-949-016-16480						
Query Match 4.1%; Score 38.6; DB 4; Length 225127;						
Best Local Similarity 54.6%; Pred. No. 1.8;						
Matches 77; Conservative 0; Mismatches 64; Indels 0; Gaps 0;						
QY	202	TGTTATGTAAACCCCTCGGGGAATCAATTAATTCATTGTTTATACAGTCTCTTCTATAT	261			
DB	125260	TTTTATGCGAAAACACTCAGTTCACAACGATCATATATTCATTATTTTTTCTATCT	125201			
QY	262	AGTGCAGAAGATCATGTTAAATAAATCTACAGGCGAGATGTAGTTTTCCTTC	321			
DB	125200	GACATACATGAGAAATGTTTCATAATTCACAAAAATTTATTAATAAGTTTATATTT	125141			
QY	322	TCAAGCAAATTCAGTGCTGT	342			
DB	125140	CCATGCAGACTTTTGTCTAT	125120			
RESULT 5						
US-09-543-681A-1767/c						
Sequence 1767, Application US/09543681A						
Patent No. 6605709						
GENERAL INFORMATION:						
APPLICANT: GARY BRETON						
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS						
FILE REFERENCE: 2709.1002-001						
CURRENT APPLICATION NUMBER: US/09/543,681A						
CURRENT FILING DATE: 2000-04-05						
PRIOR APPLICATION NUMBER: US 60/128,706						
PRIOR FILING DATE: 1999-04-09						
NUMBER OF SEQ ID NOS: 8344						
SEQ ID NO 1767						
LENGTH: 285						
TYPE: DNA						
ORGANISM: Proteus mirabilis						
US-09-543-681A-1767						
Query Match 4.0%; Score 37.8; DB 4; Length 285;						
Best Local Similarity 53.8%; Pred. No. 0.033;						
Matches 78; Conservative 0; Mismatches 67; Indels 0; Gaps 0;						
QY	237	TATGTTTATACAGTCTCTTCTATATAAGTCAGAGAAATCATGTTTAAATAAATCTACAGG	296			
DB	259	TATTAGCATCTCTCTTTCTTTATAAAGAACCACTTTTATCTTTAATATATGCAGAA	200			
QY	297	GCAGGATTGTAGTTTTTCTTCCTTCCTCACGAACTTCAGTGTGTCAGATAAATCTTCC	356			

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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12896
; LENGTH: 451924
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12896

Query Match      3.8%; Score 36.2; DB 4; Length 451924;
Best Local Similarity 50.3%; Pred. No. 20;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 225 AATGAATGAAATATGTTTATACAGTTCTTTTCTATATAAGTCAGAGAAGATCATGTTAAA 284
Db 251465 AGTGAACAAAGATAGTTTCTAGATTACAAGGTATCAAAATCATTTTCATCGGAAGT 251406

QY 285 TAAATCTACAGGCAGGATGTTAGTTTTCTCTTCAAGCAAACTTCAGTGTGTGCA 344
Db 251405 GAAATATAAGGACATAAAGGATAGTTTAATGCTGTTTAACTATAAATACTGTCA 251346

QY 345 GATAACTCTCCATGTGTTTTTTTTTTCTTAGAATGAGCCCTTCCGTGAGAACCCC 401
Db 251345 CATAAATTCATAATTGAAATTTTGTGTAATAAGTCCTGTACCTACTGGACTAGCCC 251289

RESULT 8
US-09-949-016-17305/c
; Sequence 17305, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17305
; LENGTH: 451925
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17305

Query Match      3.8%; Score 36.2; DB 4; Length 451925;
Best Local Similarity 50.3%; Pred. No. 20;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 225 AATGAATGAAATATGTTTATACAGTTCTTTTCTATATAAGTCAGAGAAGATCATGTTAAA 284
Db 251465 AGTGAACAAAGATAGTTTCTAGATTACAAGGTATCAAAATCATTTTCATCGGAAGT 251406

QY 285 TAAATCTACAGGCAGGATGTTAGTTTTTCTCTCAAGCAAACTTCAGTGTGTGCA 344
Db 251405 GAAATATAAGGACATAAAGGATAGTTTAATGCTGTTTAACTATAAATACTGTCA 251346

QY 345 GATAACTCTCCATGTGTTTTTTTTTTCTTAGAATGAGCCCTTCCGTGAGAACCCC 401
Db 251345 CATAAATTCATAATTGAAATTTTGTGTAATAAGTCCTGTACCTACTGGACTAGCCC 251289

RESULT 9
US-09-949-016-17433
; Sequence 17433, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

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APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 17433
 LENGTH: 101349
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-17433

Query Match 3.8%; Score 35.8; DB 4; Length 101349;
 Best Local Similarity 49.7%; Pred. No. 9.5;
 Matches 91; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
 72 CAAGAAATACATAGTCTGAGGATAGGAGCTGTTCAGTCTGCTAGGAGGACACAAA 131
 18199 CTAGTAATCTGAGTACCCAAATGGAACAGTTTAAATTTGAATATATAGCTTAAA 18258
 132 GCACAGACCCAGACTACAATGGGTATGAACCCCTGCGAGCTTTGTTGCCATCC 191
 18259 AAAAGAGCTCAATCACCATAGGAACATCAGAAATTTTGCATCTCCCTTAATGTTAGCC 18318
 192 TTGCCAAGCTGTATGTAAACCTCCGGGGGAATGAATGAATTAATGTTATACAGTT 251
 18319 TTAGTATTGTTTATTTAATGATTCGATATTCGAGGAGGATCATATTTTTCATG 18378
 252 CTT 254
 18379 CTT 18381

RESULT 10
 US-09-949-016-12617/c
 Sequence 12617, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 12617
 LENGTH: 160018
 TYPE: DNA
 ORGANISM: Human
 NAME/KEY: misc feature
 LOCATION: (1)-(160018)
 OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-12617

Query Match 3.7%; Score 35.6; DB 4; Length 160018;
 Best Local Similarity 50.0%; Pred. No. 15;
 Matches 89; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

234 AATTATGTTTATACAGTCTTTCTATATAAGTCGAGAAATCATGTTAAATAATCTAC 293
 33183 AGGAATTCATATATATATGCGCTTATTAGAAATCTGTATAATGATGCTTCTATCTAT 33124
 294 AGGGCAGGATTTAGTATTTTCTCTTCTCAAGCAAACTTCAGTCTCTCAGATAACTTC 353
 33123 CTCTCAAGCTTCATCTCAATACATCTCTCTAGCTCTCTGTTCTACAGCCACACCTTC 33064
 354 TCCATGTTGTTTTTTTTTCTTTAGAAAGAGCCCTTCTGAGAACCCCTCGGAATAGT 411
 33063 TTTCAGTCTCTTTTTTTTTTTTGAATAGAGTCTCCCTCTGTCCACCCAGGCTGTAGT 33006
 RESULT 11
 US-09-949-016-15994/c
 Sequence 15994, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 15994
 LENGTH: 160018
 TYPE: DNA
 ORGANISM: Human
 NAME/KEY: misc feature
 LOCATION: (1)-(160018)
 OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-15994

Query Match 3.7%; Score 35.6; DB 4; Length 160018;
 Best Local Similarity 50.0%; Pred. No. 15;
 Matches 89; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
 234 AATTATGTTTATACAGTCTTTCTATATAAGTCGAGAAATCATGTTAAATAATCTAC 293
 33183 AGGAATTCATATATATGCGCTTATTAGAAATCTGTATAATGATGCTTCTATCTAT 33124
 294 AGGGCAGGATTTAGTATTTTCTCTTCTCAAGCAAACTTCAGTCTCTCAGATAACTTC 353
 33123 CTCTCAAGCTTCATCTCAATACATCTCTCTAGCTCTCTGTTCTACAGCCACACCTTC 33064
 354 TCCATGTTGTTTTTTTTTCTTTAGAAAGAGCCCTTCTGAGAACCCCTCGGAATAGT 411
 33063 TTTCAGTCTCTTTTTTTTTTTTGAATAGAGTCTCCCTCTGTCCACCCAGGCTGTAGT 33006
 RESULT 12
 US-08-998-416-224/c
 Sequence 224, Application US/08998416
 Patent No. 6239264
 GENERAL INFORMATION:
 APPLICANT: Philippsen, Peter
 APPLICANT: Pohlmann, Rainer
 APPLICANT: Steiner, Sabine
 APPLICANT: Mohr, Christine
 APPLICANT: Wendland, Jurgen
 APPLICANT: Knechtle, Philipp
 APPLICANT: Reibschung, Corinne
 TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPIL

```

; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cortwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 224:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 782 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1208UP
; US-08-998-416-224

Query Match 3.7%; Score 35.4; DB 3; Length 782;
Best Local Similarity 53.6%; Pred. No. 0.44; Indels 2; Gaps 1;
Matches 96; Conservative 0; Mismatches 81;

Qy 205 TATGTAAACCTCCGGGGGAATGAATGAAATATGTTTATACAGTCTCTTCTATATAAG 264
Db 410 TAATTATATATATACAGGGAGTAAATTAATATATATAAATTAATTAATATACAC 351
Qy 265 TGCAGAGAATCATGTTAAATAAATCTACAGGGCAGGATGTTAGTTTTCTCTCTCA 324
Db 350 TTAATATTAATAAACTTAA--TAATCTATTTTAAATAAATAATGATATTAATATA 293
Qy 325 AGCAAACTTCAGTGTGTGACATACTCTCCATGCTGTTTTTTTCTCTTAGAATCA 383
Db 292 AATTAAATTAATACTATTATTAATAAATATCTATAAGTAATTTCTTATTATTATAA 234

RESULT 13
US-09-949-016-84673/c
; Sequence 84673, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NO 15638
; LENGTH: 69764
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(69764)
; OTHER INFORMATION: n = A,T,C or G
; US-09-949-016-15638

Query Match 3.7%; Score 35.2; DB 4; Length 69764;
Best Local Similarity 54.7%; Pred. No. 12;
Matches 70; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 153 GGGTATGAAACCCCTCTCCAGCCCTTTTGTGTCCATCCCTTGCCAAAGCTGTTATGAAA 212
Db 1765 GTGTCTGTGCTCACTTTGGAGCTTAGCATGTGCTCCCGCCGGCGTTAGGAAGTGAC 1706
Qy 213 ACCCTCCGGGGGAATGAATGAAATATGTTTATACAGTCTCTTCTATATAAGTCAGAG 272
Db 1705 CAAAGGGTGGGGAAGAATGAATATTTTAAAAAATGATTTGGCCATACTGGAGAGG 1646
Qy 273 AATCATGT 280
Db 1645 CTTCATGT 1638

RESULT 15
US-09-949-016-11852/c
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84673
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-84673

Query Match 3.7%; Score 35.2; DB 4; Length 601;
Best Local Similarity 52.0%; Pred. No. 0.42;
Matches 79; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 395 GAACCCCTCGGAATAGTAACCTACAGTACCCCAACCCAGCCAGCCATTGAGGTAACCCCTG 454
Db 599 GAATCCTGCACATTTGGAGAACAAATACTAACTCAACTGTAATGCTGAAGTCTTT 540
Qy 455 ACTCATATCTGCTCTCTCAGACACAAACCAATTTCCACCTCCAGGGGCTGGGTGTGTT 514
Db 539 ACCCACTTTCTCTCACCCCTGACAGAAAGGTTTACTCCCGAAATGGGTTGGGGGATGGG 480
Qy 515 ACAGGTTTTCAGAGTATTCACTGAAGCAGAAAT 546
Db 479 GCATGAGAACAGTGTCTTTTAAATCGTAAT 448

RESULT 14
US-09-949-016-15638/c
; Sequence 15638, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NO 15638
; LENGTH: 69764
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(69764)
; OTHER INFORMATION: n = A,T,C or G
; US-09-949-016-15638

Query Match 3.7%; Score 35.2; DB 4; Length 69764;
Best Local Similarity 54.7%; Pred. No. 12;
Matches 70; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 153 GGGTATGAAACCCCTCTCCAGCCCTTTTGTGTCCATCCCTTGCCAAAGCTGTTATGAAA 212
Db 1765 GTGTCTGTGCTCACTTTGGAGCTTAGCATGTGCTCCCGCCGGCGTTAGGAAGTGAC 1706
Qy 213 ACCCTCCGGGGGAATGAATGAAATATGTTTATACAGTCTCTTCTATATAAGTCAGAG 272
Db 1705 CAAAGGGTGGGGAAGAATGAATATTTTAAAAAATGATTTGGCCATACTGGAGAGG 1646
Qy 273 AATCATGT 280
Db 1645 CTTCATGT 1638

RESULT 15
US-09-949-016-11852/c
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us-09-778-961-3_copy_12201_13150.rni

Mon Mar 28 09:43:28 2005

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; Sequence 11852, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11852
; LENGTH: 321022
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(321022)
; OTHER INFORMATION: n = A,T,C or G
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US-09-949-016-11852

Query Match      3.7%; Score 35.2; DB 4; Length 321022;
Best Local Similarity 52.0%; Pred. No. 34;
Matches 79; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 395 GAACCCCTCGGATAGTAACTACACGTACCCCAAGCCAGCCCAATTGAGGTAAACCCCTG 454
Db 50388 GAATCTGCACATTTGGAGAACACAAATACTAACTCAACTGTAATGCTGAAGTCCTTT 50329

QY 455 ACTCACATCTGCTCTCTCAGACACAAACCATTTCACCTGCCAGGGGCTCGGGGTGGT 514
Db 50328 ACCCACTTCTCCTCACCCTGACAGAAAGGTTTACTCCGAAATGGTTGGGGGATGGG 50269

QY 515 ACAGGTTTCAGAGTATTCTACTGAAGCAGAAAT 546
Db 50268 GCATGAGAACAGTCTCTTTAAATCGTAAT 50237
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Search completed: March 27, 2005, 03:59:08
Job time : 173.092 secs

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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 22:06:11 ; Search time 550.168 Seconds
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Perfect score: 950
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Scoring table: IDENTITY_NUC
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Maximum Match 100%
Listing first 45 summaries

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- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	70	7.4	572	10	US-09-764-891-1391
2	70	7.4	802	17	US-10-276-774-73
3	70	7.4	802	17	US-10-296-115-600
4	70	7.4	4268	17	US-10-092-900A-81
5	70	7.4	4377	13	US-10-054-691-1
6	70	7.4	4424	18	US-10-478-245-19
7	70	7.4	4425	17	US-10-092-900A-85
8	70	7.4	4607	18	US-10-478-245-11
9	41.6	4.4	5506	9	US-09-967-552A-73
10	41.6	4.4	13031	16	US-10-387-894-5
11	41	4.3	2339	18	US-10-437-963-17333

c	12	38.6	4.1	816	17	US-10-282-122A-18201	Sequence 18201, A
	13	38.6	4.1	3673778	16	US-10-312-841-2	Sequence 2, Appli
	14	38	4.0	2031	17	US-10-094-749-774	Sequence 774, App
	15	37.4	3.9	424	9	US-09-960-352-14786	Sequence 14786, A
	16	37.4	3.9	13712	15	US-10-311-455-1504	Sequence 1504, Ap
	17	37.2	3.9	9733	15	US-10-311-455-655	Sequence 655, App
	18	36.8	3.9	900	16	US-10-203-754A-36	Sequence 36, Appl
	19	36.8	3.9	900	16	US-10-203-754A-37	Sequence 37, Appl
	20	36.8	3.9	900	16	US-10-203-754A-38	Sequence 38, Appl
	21	36.8	3.9	900	16	US-10-203-754A-62	Sequence 62, Appl
	22	36.8	3.9	900	16	US-10-203-754A-64	Sequence 64, Appl
	23	36.8	3.9	900	16	US-10-203-754A-65	Sequence 65, Appl
	24	36.8	3.9	903	16	US-10-203-754A-39	Sequence 63, Appl
	25	36.4	3.9	915	16	US-10-203-754A-39	Sequence 39, Appl
	26	36.4	3.8	63502	13	US-10-087-192-271	Sequence 271, App
	27	36.2	3.8	788	15	US-10-278-845-31	Sequence 31, Appl
	28	36.2	3.8	905	15	US-10-278-845-8	Sequence 8, Appli
	29	36	3.8	1730	17	US-10-369-493-29357	Sequence 29357, A
	30	36	3.8	2285	17	US-10-094-749-1312	Sequence 1312, Ap
	31	36	3.8	684187	18	US-10-367-094-71	Sequence 71, Appl
	32	35.8	3.8	223	17	US-10-424-599-117628	Sequence 117628,
	33	35.8	3.8	458	10	US-09-918-995-26975	Sequence 26975, A
	34	35.8	3.8	160820	18	US-10-473-939-5	Sequence 5, Appli
	35	35.8	3.8	3673778	16	US-10-312-841-1	Sequence 1, Appli
	36	35.8	3.7	1329	17	US-10-425-114-9068	Sequence 9068, Ap
	37	35.6	3.7	1347	17	US-10-424-599-57419	Sequence 57419, A
	38	35.6	3.7	47777	19	US-10-741-600-17649	Sequence 17649, A
	39	35.6	3.7	52677	13	US-10-087-192-130	Sequence 130, App
	40	35.6	3.7	1950	13	US-10-027-632-99132	Sequence 99132, A
	41	35.4	3.7	1950	17	US-10-027-632-99132	Sequence 99132, A
	42	35.4	3.7	5735	17	US-10-257-166-147	Sequence 147, App
	43	35.4	3.7	428	14	US-10-184-644-514	Sequence 514, App
	44	35.2	3.7	428	14	US-10-184-644-514	Sequence 514, App
	45	35.2	3.7	428	14	US-10-184-644-514	Sequence 514, App

ALIGNMENTS

RESULT 1
US-09-764-891-1391
; Sequence 1391, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1391
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (375)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (529)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-891-1391

Query Match 7.4%; Score 70; DB 10; Length 572;
Best Local Similarity 93.6%; Pred. No. 3.7e-11;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 367 TTTTCTCTTAGATGAGCCCTTCCTGAGAACCCCTCGGAATAGTACTACCTACCC 426
Db 91 TGTCCCACTCAGATGAGCCCTTCCTGAGAACCCCTCGGAATAGTACTACCTACCC 150

Mon Mar 28 09:43:28 2005

QY 427 ATCAAGCCAGCCATTGAG 444
|
Db 151 ATCAAGCCAGCCATTGAG 168

RESULT 2
US-10-276-774-73
; Sequence 73, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hvaeq, Inc.
; APPLICANT: Tang, Y. Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276, 774
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560, 875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496, 914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 73
; LENGTH: 802
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-73

Query Match 7.4%; Score 70; DB 17; Length 802;
Best Local Similarity 93.6%; Pred. No. 4.5e-11;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 367 TTTTCTCTTAGAATGAGCCCTTCTCGAAGACCCCTCGGAATAGTAACGTACGACCC 426
Db 195 TGTCCACTCAGATGAGCCCTTCTCGAAGACCCCTCGGAATAGTAACGTACGACCC 254

QY 427 ATCAAGCCAGCCATTGAG 444
|
Db 255 ATCAAGCCAGCCATTGAG 272

RESULT 3
US-10-296-115-600
; Sequence 600, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hvaeq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT.
; CURRENT APPLICATION NUMBER: US/10/296, 115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552, 317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 600
; LENGTH: 802
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-600

Query Match 7.4%; Score 70; DB 17; Length 802;
Best Local Similarity 93.6%; Pred. No. 4.5e-11;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 367 TTTTCTCTTAGAATGAGCCCTTCTCGAAGACCCCTCGGAATAGTAACGTACGACCC 426
Db 195 TGTCCACTCAGATGAGCCCTTCTCGAAGACCCCTCGGAATAGTAACGTACGACCC 254
QY 427 ATCAAGCCAGCCATTGAG 444
|
Db 255 ATCAAGCCAGCCATTGAG 272

RESULT 4
US-10-092-900A-81
; Sequence 81, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev, Vellizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092, 900A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USSN 60/274, 322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/283, 675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USSN 60/338, 092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USSN 60/274, 281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/274, 191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USSN 60/325, 681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USSN 60/304, 354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USSN 60/279, 995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USSN 60/294, 899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USSN 60/287, 424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 81
; LENGTH: 4268
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4258)
US-10-092-900A-81

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Query Match 7.4%; Score 70; DB 17; Length 4268;
Best Local Similarity 93.6%; Pred. No. 1.2e-10;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 367 TTTTCTCTTAGAATGAGCCCTTCTCGAGAACCCCTCGGAATAGTAACGTACACGTACCC 426
Db 3016 TGTCCACTCAGATGAGCCCTTCTCGAGAACCCCTCGGAATAGTAACGTACACGTACCC 3075

OY 427 ATCAAGCCAGCCATTGAG 444
Db 3076 ATCAAGCCAGCCATTGAG 3093

RESULT 5
US-10-054-691-1
; Sequence 1, Application US/10054691
; Publication No. US20020115846A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020115846A1el Human Lipase and Polynucleotides Encoding
; FILE REFERENCE: LEX-0303-USA
; CURRENT APPLICATION NUMBER: US/10/054,691
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 60/264,049
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4377
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-054-691-1

Query Match 7.4%; Score 70; DB 13; Length 4377;
Best Local Similarity 93.6%; Pred. No. 1.2e-10;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 367 TTTTCTCTTAGAATGAGCCCTTCTCGAGAACCCCTCGGAATAGTAACGTACACGTACCC 426
Db 3118 TGTCCACTCAGATGAGCCCTTCTCGAGAACCCCTCGGAATAGTAACGTACACGTACCC 3177

OY 427 ATCAAGCCAGCCATTGAG 444
Db 3178 ATCAAGCCAGCCATTGAG 3195

RESULT 6
US-10-478-245-19
; Sequence 19, Application US/10478245
; Publication No. US20040171009A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;
; APPLICANT: YUE, Henry; AZIMZAI, Yalda;
; APPLICANT: BAUGHN, Mariah R.; BURFORD, Neil;
; APPLICANT: REDDY, Roopa; CHAWLA, Narinder K.;
; APPLICANT: DAS, Debopriya; NGUYEN, Darniel B.;
; APPLICANT: YAO, Monique G.; ARVIZU, Chandra S.;
; APPLICANT: LU, Yan; GANDHI, Ameena R.;
; APPLICANT: GRIFFIN, Jennifer A.; ELLIOTT, Vicki S.;
; APPLICANT: RAMKUMAR, Javalaxmi; LAL, Preeti G.;
; APPLICANT: LU, Dyung Aina M.; LEE, Ernestine A.;
; APPLICANT: LEE, Soo Y.; YUE, Huibin;
; APPLICANT: YANG, Junning; TRIBOULEY, Catherine M.;
; APPLICANT: KABLE, Amy E.; SWARNAKAR, Anita
; TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES
; FILE REFERENCE: PI-0427 USN
; CURRENT APPLICATION NUMBER: US/10/478,245
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/15688
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/292,242

; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/293,726
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/295,346
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/303,404
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 60/314,754
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/351,262
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/368,799
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 4424
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7504684CB1
US-10-478-245-19

Query Match 7.4%; Score 70; DB 18; Length 4424;
Best Local Similarity 93.6%; Pred. No. 1.2e-10;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 2939 TGTCCACTCAGATGAGCCCTTCTCGAGAACCCCTCGGAATAGTAACGTACACGTACCC 2998

OY 427 ATCAAGCCAGCCATTGAG 444
Db 2999 ATCAAGCCAGCCATTGAG 3016

RESULT 7
US-10-092-900A-85
; Sequence 85, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhuseen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsbrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
```

Mon Mar 28 09:43:28 2005

TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-290C
CURRENT APPLICATION NUMBER: US/10/092,900A
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: USSN 60/274,322
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USSN 60/283,675
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: USSN 60/338,092
PRIOR FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: USSN 60/274,281
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USSN 60/274,191
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USSN 60/325,681
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: USSN 60/304,354
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: USSN 60/279,995
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: USSN 60/294,899
PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: USSN 60/287,424
PRIOR FILING DATE: 2001-04-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 768
SEQ ID NO 85
LENGTH: 4425
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (16)...(4285)
US-10-092-900A-85

Query Match 7.4%; Score 70; DB 17; Length 4425;
Best Local Similarity 93.6%; Pred. No. 1.2e-10; Indels 0; Gaps 0;
Matches 73; Conservative 0; Mismatches 5

QY 367 TTTTCTCTTAGAATGAGCCCTTCTCGAGAACCCCTCGGAATAGTAACTACAGTACCC 426
DB 3040 TGTCCCACTCAGAAATGAGCCCTTCTCGAGAACCCCTCGGAATAGTAACTACAGTACCC 3099
QY 427 ATCAAGCCAGCCATTGAG 444
DB 3100 ATCAAGCCAGCCATTGAG 3117

RESULT 8
US-10-478-245-11
Sequence 11, Application US/10478245
Publication No. US20040171009A1
GENERAL INFORMATION:
APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;
APPLICANT: YUE, Henry; AZIMZAI, Valda;
APPLICANT: BAUGHN, Mariah R.; BURFORD, Neil;
APPLICANT: REDDI, Roopa; CHAWLA, Narinder K.;
APPLICANT: DAS, Debopriya; NGUYEN, Daniel B.;
APPLICANT: YAO, Monique G.; ARVIZU, Chandra S.;
APPLICANT: LU, Yan; GANDHI, Ameena R.;
APPLICANT: GRIFFIN, Jennifer A.; ELLIOTT, Vicki S.;
APPLICANT: RAMKUMAR, Javalaxmi; LAL, Preeti G.;
APPLICANT: LU, Dzung Aina M.; LEE, Ernestine A.;
APPLICANT: LEE, Soo Y.; YUE, Huibin;
APPLICANT: YANG, Junning; TRIBOULEY, Catherine M.;
APPLICANT: KABLE, Amy E.; SWARNAKAR, Anita
TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES
FILE REFERENCE: PI-0427 USN
CURRENT APPLICATION NUMBER: US/10/478,245
CURRENT FILING DATE: 2003-11-18
PRIOR APPLICATION NUMBER: PCT/US02/15688
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: US 60/292,242

PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/293,726
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/295,346
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: US 60/303,404
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US 60/314,754
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/351,262
PRIOR FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 60/368,799
PRIOR FILING DATE: 2002-03-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PERL Program
SEQ ID NO 11
LENGTH: 4607
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 2440624CB1
US-10-478-245-11

Query Match 7.4%; Score 70; DB 18; Length 4607;
Best Local Similarity 93.6%; Pred. No. 1.2e-10; Indels 0; Gaps 0;
Matches 73; Conservative 0; Mismatches 5

QY 367 TTTTCTCTTAGAATGAGCCCTTCTCGAGAACCCCTCGGAATAGTAACTACAGTACCC 426
DB 3126 TGTCCCACTCAGAAATGAGCCCTTCTCGAGAACCCCTCGGAATAGTAACTACAGTACCC 3185
QY 427 ATCAAGCCAGCCATTGAG 444
DB 3186 ATCAAGCCAGCCATTGAG 3203

RESULT 9
US-09-967-552A-73/c
Sequence 73, Application US/09967552A
Patent No. US20020124282A1
GENERAL INFORMATION:
APPLICANT: Danilevskaya, Olga
APPLICANT: Butler, Karlene H.
APPLICANT: Miao, Guo-Hua
APPLICANT: Morgante, Michele
APPLICANT: Sakai, Hajime
APPLICANT: Simmons, Carl R.
APPLICANT: Weng, Zude
APPLICANT: Famodu, Omolayo
APPLICANT: Hantke, Sabine
TITLE OF INVENTION: Plant Reproduction Polynucleotides and Methods of Use
FILE REFERENCE: DD0010R
CURRENT APPLICATION NUMBER: US/09/967,552A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/US00/23735
PRIOR FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: US 60/151,575
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 73
LENGTH: 5506
TYPE: DNA
ORGANISM: Zea mays
US-09-967-552A-73

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Best Local Similarity 53.8%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 86; Conservative 0; Mismatches 74

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Db 3967 GTAACCTGAATATATAAACAAGTCAAACTCATTAACCTGTGATGGTTAAGAACACCTATAC 3908
Qy 171 ACGCTTTTGTGTCCATCCCTTCCAAAGCTGTATGATAAAACCTCCGGGGGAATGAA 230
Db 3907 AACCATGCCATTGCTATGCAATCCAAACAACTTAATTCCAAACCTAGTTGAAAAGTGAA 3848
Qy 231 TGAATATTATTTATACAGTCTCTTCTATATATAAGTGCGA 270
Db 3847 TGAAGAGAAGAGAAAAAAGAACTTAGTATCTAACTATACA 3808

RESULT 10

US-10-387-894-5/c
; Sequence 5, Application US/10387894
; Publication No. US20030177547A1
; GENERAL INFORMATION:
; APPLICANT: Danilevskaya, Olga
; TITLE OF INVENTION: Imprinting in Plants to Control Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 1487
; CURRENT APPLICATION NUMBER: US/10/387,894
; CURRENT FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US 60/363,861
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 13031
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (11384)...(11481)
; OTHER INFORMATION: N = A, T, C or G
US-10-387-894-5

Query Match 4.4%; Score 41.6; DB 16; Length 13031;
Best Local Similarity 53.8%; Pred. No. 0.27;
Matches 86; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
Qy 111 GTTCTAGGAGACACAAAGCAGACCCAGCTACATGCTGATGAACCTCTGC 170
Db 3967 GTAACCTGAATATATAAACAAGTCAAACTCATTAACCTGTGATGGTTAAGAACACCTATAC 3908
Qy 171 ACGCTTTTGTGTCCATCCCTTCCAAAGCTGTATGATAAAACCTCCGGGGGAATGAA 230
Db 3907 AACCATGCCATTGCTATGCAATCCAAACAACTTAATTCCAAACCTAGTTGAAAAGTGAA 3848
Qy 231 TGAATATTATTTATACAGTCTCTTCTATATATAAGTGCGA 270
Db 3847 TGAAGAGAAGAGAAAAAAGAACTTAGTATCTAACTATACA 3808

RESULT 11

US-10-437-963-17333
; Sequence 17333, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 17333
; LENGTH: 2339
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(2339)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_22997C.1
US-10-437-963-17333

Query Match 4.3%; Score 41; DB 18; Length 2339;
Best Local Similarity 54.2%; Pred. No. 0.15;
Matches 83; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
Qy 682 TTCTTTGACCTTGGCAATCTCTGGCTCACAGAGCTGTTACTCTTAGGCAGCTCAGCC 741
Db 133 TTCTTTTCCACACAGAGCGGGCGGAGACAGGTCCCGGAACCTTGGCGGAGCGCG 192
Qy 742 TCTCAAGAGGAGGAGGAGCTGTGTGATGTGGCGTTGACTTTTGAAGGTGGAGCTG 801
Db 193 GCTCAAGCGCAGGTCAAAAGGGGTGAGTGGCGTCTGCTCGTGGGCGCGCGG 252
Qy 802 AGTGGAGGGAACCTACAAATTTCTGGGATGGAC 834
Db 253 CGCGCGCTGGCTTTCACGCGGGCGGGGC 285

RESULT 12

US-10-282-122A-18201/c
; Sequence 18201, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1

[illegible]

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Job time : 559.168 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 13:10:00 ; Search time 3061.72 Seconds
(without alignments)
11810.698 Million cell updates/sec

Title: US-09-778-961-3_COPY_12201_13150

Perfect score: 950

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1.*
2: gb_est2.*
3: gb_hc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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3	70	7.4	491	4	BM149001	BM149001 TCAAP2E57
4	70	7.4	587	2	AW752833	AW752833 IL3-CT022
5	70	7.4	763	4	BL912073	BL912073 603068631
6	70	7.4	823	4	BL488437	BL488437 603020936
7	70	7.4	880	4	BL912651	BL912651 603290988
8	70	7.4	921	5	BX354650	BX354650 BX354650
9	70	7.4	1081	5	BM923066	BM923066 AGENCOURT
10	70	7.4	1661	3	CH612785	CH612785 full-leng
11	68.4	7.2	1033	4	BM549919	BM549919 AGENCOURT
12	66.8	7.0	608	2	AW851123	AW851123 IL3-CT022
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C 14	42.6	4.5	636	1	AA637588	AA637588 vr28f11.i
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C 16	41.6	4.4	874	7	CO232246	CO232246 WS00725.B
C 17	41	4.3	879	7	CK019498	CK019498 AGENCOURT
C 18	40.8	4.3	943	9	BN246070	BN246070 Danio rer
19	40.8	4.3	943	9	CNS002IM	AL097720 Drosophil
20	40.4	4.3	704	8	CC308163	CC308163 TAM32-1A1
21	40.4	4.3	1162	9	AG361195	AG361195 Mus muscu
22	40.4	4.3	1169	8	CC206063	CC206063 CH261-122
C 23	40.2	4.2	982	8	CC274437	CC274437 CH261-132
C 24	40	4.2	202	6	C90343	C90343 C90343 Dict

25	39.8	4.2	663	9	BX182777	BX182777 Danio rer
26	39.8	4.2	696	9	BX183050	BX183050 Danio rer
27	39.8	4.2	708	9	BX247380	BX247380 Danio rer
28	39.6	4.2	393	8	AQ488465	AQ488465 RPCI-11-2
C 29	39.6	4.2	625	9	CL701053	CL701053 SP_Ba006
C 30	39.6	4.2	914	9	CNS002JY	AL097768 Drosophil
C 31	39.4	4.1	716	9	BX184059	BX184059 Danio rer
C 32	39.4	4.1	830	9	BX180731	BX180731 Danio rer
C 33	39.2	4.1	541	8	BH009019	BH009019 ef22g11.x
C 34	39.2	4.1	550	7	CN473609	CN473609 USDA-FP.1
C 35	39.2	4.1	814	9	CNS008BT	AL051475 Drosophil
C 36	39	4.1	858	6	CA792141	CA792141 AGENCOURT
C 37	38.8	4.1	664	1	AJ741338	AJ741338 AJ741338
C 38	38.8	4.1	1861	4	BG035775	BG035775 602325858
C 39	38.6	4.1	1025	9	CNS00A1Z	AL055840 Drosophil
C 40	38.4	4.0	629	6	CD471124	CD471124 LeukoS5.4
C 41	38.4	4.0	649	9	AG572132	AG572132 Mus muscu
C 42	38.4	4.0	770	8	BH487663	BH487663 BOHGU54TF
C 43	38.4	4.0	861	8	BZ608381	BZ608381 WHACF66TR
C 44	38.2	4.0	776	9	CC906457	CC906457 t029b19ba
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ALIGNMENTS

RESULT 1
BH069515/c
LOCUS RPCI-24-214P9.TV RPCI-24 460 bp DNA linear GSS 18-JUL-2001
DEFINITION genomic survey sequence.
ACCESSION BH069515
VERSION BH069515.1 GI:14889112
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 460)
AUTHORS Zhao S., Nierman W., Malek J., Shatman S., Akinret B., Levins M.,
Tsegaye G., Geer K., Krol M., Shvartsbeyn A., Gebregorgis E.,
Russell B., de Jong P. and Fraser C.M.
TITLE Mouse BAC End Sequences from Library RPCI-24
JOURNAL Unpublished (1999)
COMMENT Other GSSs: RPCI-24-214P9.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.choi.org). Clones may be purchased from BACPAC
Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 214 row: P column: 9
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .460
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-214P9"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/notes="Vector: pTARBAC1; Site_1: BamHI; Site_2: BamHI;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the

ORIGIN

Query Match 9.2%; Score 87.2; DB 8; Length 460;
Best Local Similarity 59.2%; Pred. No. 5.8e-14;
Matches 213; Conservative 0; Mismatches 128; Indels 19; Gaps 3;

QY 462 TCTGCTCTCTAGACACAAACATTTCCACTGCGCAGGGG-TCGGGTGGGTACAGGT 520
DB 460 TCTGCTCTCTTAGACACAAAGTCAGTCCACCTGCGCAGGGACTTGGGGTGGGTCCAGAT 401

QY 521 TTCAAGTATTTCACTGAAGCAGAAATGTACTTCTTACATACCTGGGATTTGGAATGTACAG 580
DB 400 TTCACTGTAGTTAAGCACAAGTATACCACTTACATACCTGGGAATTTGGAATGTACAA 341

QY 581 AAA-----AGGTCCTCGGACCAAGCAAGCCAGGATTCCTTAAACATGTT 625
DB 340 AAACACAAAAAACAAGCAAAACAACTGGAACCTAAGGCCCCAGAAATAGTCTGACTTGT 281

QY 626 CTCAAGTGTCTACCTGACCTGAGCCCCCAAGCAGAGGAAGTGTCTATGATCGATTTTC 685
DB 280 CTCAAGTGTCCACCTGATGTCTGCTCTCAGAGACATTTGTTTCAATTAACACAGCTTAGCCTTAC 164

QY 686 TTTCACCTTGGCAATCTCTGGGCTACAGAGCTGGTTACTGCTTAGCAGCTAGCCTCTC 745
DB 223 TGTGACCTGACCTTGTCTGCTCTCAGAGACATTTGTTTCAATTAACACAGCTTAGCCTTAC 164

QY 746 AAGAGGAGAGGAGCTGCTGTGATGTCGGCTTCTCTTCTGGAAGCTGAGGCTGAGTG 805
DB 163 AAGATCAAGATAGCAGGGATAAGGAGAGTAGGTATAGTGTTCAGGGTGGGCGAGGGG 104

RESULT 2

AA418228 265 bp mRNA linear EST 16-OCT-1997
LOCUS z937h09.r1 Soares NHMPu_S1 Homo sapiens cDNA clone IMAGE:767777 5'
DEFINITION similar to SW:PHLX_RABIT_Q05017 PHOSPHOLIPASE ADRAB-B PRECURSOR ; mRNA sequence.

ACCESSION AA418228
VERSION AA418228.1 GI:2080047
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
AUTHORS WashU-Merck EST Project 1997
TITLE Unpublished (1997)
JOURNAL Unpublished (1997)
COMMENT Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 178.
Location/Qualifiers
1. .265
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/clone="IMAGE:767777"
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/lab_host="DH10B"
/clone_lib="Soares_NHMPu_S1"

ORIGIN

Query Match 7.4%; Score 70; DB 1; Length 265;
Best Local Similarity 93.6%; Pred. No. 5.7e-09;
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 367 TTTTTCCTCTAGATGAGCCCTTCTCTGAGAACCCCTCGGATAGTAACTACACGTACCCC 426
DB 91 TGTCCCACTCAGAATGAGCCCTTCTCTGAGAACCCCTCGGATAGTAACTACACGTACCCC 150

QY 427 ATCAAGCAGCCATTGAG 444
DB 151 ATCAAGCAGCCATTGAG 168

RESULT 3

BM149001 491 bp mRNA linear EST 30-NOV-2001
LOCUS TCAAP2E5701 Pediatric acute myelogenous leukemia cell (FAB M1)
DEFINITION Baylor-HGSC project-TCAA Homo sapiens cDNA clone TCAAP5701, mRNA sequence.

ACCESSION BM149001
VERSION BM149001.1 GI:17170225
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Wei, Y., Tsang, Y.-T.M., Mei, G., Ku, J.M., Ali-Osman, F.R. Jr., Gunaratne, P.H., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.P.
AUTHORS Pediatric Leukemia cDNA Sequencing Project (2001)
TITLE Unpublished (2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Tel: 832-824-4536
Fax: 832-825-4038
Email: clones@tccc.org
Seq primer: M13 primer.
Location/Qualifiers
1. .491
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TCAAP5701"
/sex="male"
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/cell_type="myeloid cell"
/dev_stage="pediatric 6 years"
/lab_host="DH10B"
/clone_lib="Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project-TCAA"
/notes="Vector: lambda pSB; Site 1: BamHI; Site 2: EcoRI; First strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GGAGACTCGAGCGCCGCGAGGAG(T)VN 3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand was primed with a BamHI-dC primer [5'AGAGAGCTCGATCCGCGCCGAATAATAAT(C) 3']. Double-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and SalI sites of

stringency conditions."

Query Match 7.4%; Score 70; DB 2; Length 587;

Qy 367 TTTTCTCTTAGAATGAGCCCTTCTTGAGAACCCTCGGAATAGTAACGTACCCC 426
| | | | |
Dδ 373 TGTCCCACTCAGAATGAGCCCTTCTTGAGAACCCTCGGAATAGTAACGTACCCC 432

Db
433 ATCAAGCCAGCCATTGAG 450

RESULT 5

ACCESSION BI912073
VERSION BI912073.1 GT:16176045

ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

Email: cgapbs-i@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

around through the I.M.A.G.E. CONSOLIDUM/LEND at:
<http://image.llnl.gov>
 Plate: LLMI1546 row: n column: 07
 High quality sequence stop: 758.

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/:-763
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5217606"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NH MGC 118"

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/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_lbw="NIH MGC 118"
/notes="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb. insert size range

```

containing the average insert size of 1.1 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH MGC Library."

ORIGIN

Query Match	7.4%	Score 70;	DB 4;	Length 763;
Best Local Similarity	93.6%;	Pred. No. 7.5e-09;		
Matches 73;	Conservative	0;	Mismatch 5;	Indels 0;

367 TTTTCTCTTGAATGAGCCCTCTCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC 426
 |||||
 508 TGTCCTCACTCAGAACTGAGCCCTCTCTGAGAACCCCTCGGAATAGTAACTACACGTACCCC 567
 |||||
 427 ATCAAGCCAGCCATTGAG 444
 |||||

us-09-778-961-3_copy_12201_13150.rst

Mon Mar 28 09:43:29 2005

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Db      568 ATCAAGCCAGCCATTGAG 585

RESULT 6
BI488437
LOCUS   823 bp mRNA linear EST 28-AUG-2001
DEFINITION Homo sapiens cDNA clone IMAGE:5191712 5',
            mRNA sequence.
ACCESSION BI488437
VERSION   BI488437.1 GI:15327665
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 823)
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE     Unpublished (1999)
JOURNAL   Contact: Robert Strausberg, Ph.D.
COMMENT   Email: cgabbs-r@mail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM11479 row: g column: 09
          High quality sequence stop: 808.
          Location/Qualifiers
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     /clone="IMAGE:5191712"
     /lab_host="DH10B"
     /clone_lib="NIH_MGC_114"
     /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
           Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
           male brains, age range 23-27 yo. Library is oligo-dT
           primed and directionally cloned (EcoRV site is destroyed
           upon cloning). Average insert size 1.5 kb, insert size
           range 1-3 kb. Library is normalized and enriched for
           full-length clones and was constructed by C. Gruber
           (Invitrogen). Research Genetics tracking code 019. Note:
           this is a NIH_MGC Library."
ORIGIN
Query Match      7.4%; Score 70; DB 4; Length 823;
Best Local Similarity 93.6%; Pred. No. 7.6e-09; Indels 0; Gaps 0;
Matches 73; Conservative 0; Mismatches 5;
QY 367 TTTTCTCTTAGATGAGCCCTTCTGAGAACCCCTCGGAATAGTAAGTACACGTACCC 426
Db 207 TGTCCCACTCAGATGAGCCCTTCTGAGAACCCCTCGGAATAGTAAGTACACGTACCC 266
QY 427 ATCAAGCCAGCCATTGAG 444
Db 267 ATCAAGCCAGCCATTGAG 284

RESULT 7
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LOCUS   880 bp mRNA linear EST 16-OCT-2001
DEFINITION Homo sapiens cDNA clone IMAGE:5220333 5',
            mRNA sequence.
ACCESSION BI912651
VERSION   BI912651.1 GI:16176846
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 921)
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE     Unpublished (1999)
JOURNAL   Contact: Robert Strausberg, Ph.D.
COMMENT   Email: cgabbs-r@mail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM11553 row: o column: 22
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          High quality sequence stop: 726.
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     /clone="IMAGE:5220333"
     /tissue_type="leukocyte"
     /lab_host="DH10B"
     /clone_lib="NIH_MGC_118"
     /note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
           (destroyed); RNA source leukocytes from anonymous pool of
           non-activated adult donors. Library is oligo-dT primed
           and directionally cloned (EcoRV site is destroyed upon
           cloning). Average insert size 1.7 kb, insert size range
           1.2-3.3 kb. Library is normalized and enriched for
           full-length clones and was constructed by C. Gruber
           (Invitrogen). Research Genetics tracking code 027. Note:
           this is a NIH_MGC Library."
ORIGIN
Query Match      7.4%; Score 70; DB 4; Length 880;
Best Local Similarity 93.6%; Pred. No. 7.8e-09; Indels 0; Gaps 0;
Matches 73; Conservative 0; Mismatches 5;
QY 367 TTTTCTCTTAGATGAGCCCTTCTGAGAACCCCTCGGAATAGTAAGTACACGTACCC 426
Db 527 TGTCCCACTCAGATGAGCCCTTCTGAGAACCCCTCGGAATAGTAAGTACACGTACCC 586
QY 427 ATCAAGCCAGCCATTGAG 444
Db 587 ATCAAGCCAGCCATTGAG 604

RESULT 8
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LOCUS   921 bp mRNA linear EST 23-APR-2004
DEFINITION Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DC023YA08 5-PRIME, mRNA sequence.
ACCESSION BX354650
VERSION   BX354650.2 GI:46550126
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 921)
REFERENCE Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
AUTHORS   Full-length cDNA libraries and normalization
TITLE     Unpublished (2001)
JOURNAL   On May 5, 2003 this sequence version replaced gi:30379890.
COMMENT   Contact: Genoscope
          Genoscope - Centre National de Sequencage
          2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
          Email: seqref@genoscope.cns.fr, web: www.genoscope.cns.fr
          1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned

```


Mon Mar 28 09:43:29 2005

AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE
20202663

PUBMED
10737800

COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2=IL3-CT0220-150
200-070-H02&t3=2000-02-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 19
High quality sequence stop: 535.
Location/Qualifiers
1..608
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0220"
/note="Organ: colon; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

FEATURES
source

ORIGIN
Query Match 7.0%; Score 66.8; DB 2; Length 608;
Best Local Similarity 91.0%; Pred. No. 6.1e-08;
Matches 71; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
367 TTTTCTCTTAGAATGAGCCCTTCTGAGACCCCTCGGAATAGTAACTACACGTACCC 426
475 TGTCCCACTCAGATGAGCCCTTCTGAGACCCCTCGGAATAGTAACTACACGTACCC 534
427 ATCAAGCCAGCCATTGAG 444
535 ATCAAGCCAGCCATTGAG 552

RESULT 13
LOCUS CK950931 872 bp mRNA linear EST 15-MAR-2004
DEFINITION 409092 BAC 10BOV Bos taurus cDNA clone 10BOV27_c11 5', mRNA sequence.
ACCESSION CK950931
VERSION CK950931.1 GI:45465311
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 872)
AUTHORS Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
TITLE Production of EST from cDNA libraries derived from immunologically activated bovine gut

AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE
20202663

PUBMED
10737800

COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2=IL3-CT0220-150
200-070-H02&t3=2000-02-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 19
High quality sequence stop: 535.
Location/Qualifiers
1..608
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0220"
/note="Organ: colon; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

FEATURES
source

ORIGIN
Query Match 7.2%; Score 68.4; DB 4; Length 1033;
Best Local Similarity 92.3%; Pred. No. 2.4e-08;
Matches 72; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
367 TTTTCTCTTAGAATGAGCCCTTCTGAGACCCCTCGGAATAGTAACTACACGTACCC 426
214 TGTCCCACTCAGATGAGCCCTTCTGAGACCCCTCGGAATAGTAACTACACGTACCC 273
427 ATCAAGCCAGCCATTGAG 444
274 ATCAAGCCAGCCATTGAG 291

RESULT 12
LOCUS AW851123 608 bp mRNA linear EST 19-MAY-2000
DEFINITION IL3-CT0220-150200-070-H02 CT0220 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW851123
VERSION AW851123.1 GI:7946640
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 608)

Mon Mar 28 09:43:29 2005

Siddiqui, A., Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C.,
 Ritland, K. and Bohlmann, J.
 The spruce transcriptome: Analysis of expressed sequence tags from
 multiple cDNA libraries
 Unpublished (2004)
 Contact: Joerg Bohlmann
 Genome BC forest genomics program
 University of British Columbia
 UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237,
 Vancouver, British Columbia, Canada, V6T 1Z3
 Tel: 1-604-822-0282
 Fax: 1-604-822-6097
 Email: bohlmann@interchange.ubc.ca
 Plate: WS00816 row: C column: 04
 High quality sequence stop: 693
 POLYA=Yes.

FEATURES
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 /tissue_type="Early season xylem harvested June 15th, mid
 season xylem harvested July 10th and late season xylem
 harvested August 17th"
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 /clone_lib="WS-X-N-A-9"
 /note="Organ: Outer xylem from 25 year old trees harvested
 at Kalamalka Research Station in Vernon, British Columbia
 in 2001; Vector: pBluescript II SK (+) XR; Site 1: EcoRI
 (5' end of cDNA); Site 2: XhoI (3' end of cDNA); mRNA was
 isolated from each tissue source independently and equal
 quantities of mRNA from each tissue were then pooled. cDNA
 was prepared from 5 micrograms of mRNA and directionally
 ligated into the pBluescript II SK (+) XR vector using the
 pBluescript II XR cDNA library Construction Kit according
 to manufacturer's instructions with modifications
 (Stratagene). Plasmid DNA was then transformed by
 electroporation into DH10B cells (Invitrogen) for
 propagation. Normalization was applied according to
 published methods [Bonaldo M.F. et al. (1996) Genome
 Research 6(9):791] in order to reduce the abundance of
 highly expressed transcripts."

ORIGIN

Query Match 4.4%; Score 41.6; DB 7; Length 693;
 Best Local Similarity 53.0%; Pred. No. 1.6;
 Matches 89; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
 QY 128 AAAAGCAGACAGCCCGAGCTACATGGGTATGAACCTCTGCAGCCTTTTGTGCA 187
 Db 561 AGATCCACTGATCGGAGCAGAGAGCTATGAATCTCTGCAACGTTGATCTGA 502
 QY 188 TCCTTCCCAAGCTGTATGTAACCTCCGCGGGGATGAATGAATTTATTTATAC 247
 Db 501 AGCCAAGCAAACTGGAGGAAGATGGCAGCTCGGGGCTGAATTAATTCGTTGAA 442
 QY 248 AGTTCTTTTCTATATAGTGCAGAGATCATGTTAAATTAATCTACAG 295
 Db 441 GTCTAGGCTTAAGATGTTGGAACATTTTGTGTAATAGTATTATACAG 394

Search completed: March 27, 2005, 03:40:53
 Job time : 3067.72 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 11:21:05 ; Search time 4368.45 Seconds
(without alignments)
11092.094 Million cell updates/sec

Title: US-09-778-961-3_COPY_22051_23050
Perfect score: 1000
Sequence: 1 ataatttggtggtgcgggt.....agggaagtcctcagggga 1000

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.on.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	1000	100.0 43543 6 AX711964	AX711964 Sequence
2	982.8	98.3 163595 2 AC022076	AC022076 Homo sapi
3	974.4	97.4 180465 9 AC074011	AC074011 Homo sapi
C 4	238.6	23.9 181102 9 AC090058	AC090058 Homo sapi
5	234.4	23.4 155086 9 BS000244	BS000244 Pan trogl
6	234.4	23.4 201304 9 BS000245	BS000245 Pan trogl
7	229	22.9 82117 9 AP000338	AP000338 Homo sapi
8	229	22.9 100000 9 AP000216	AP000216 Homo sapi
C 9	229	22.9 340000 9 AP001760	AP001760 Homo sapi
C 10	213.8	21.4 143770 9 AL589987	AL589987 Human DNA
C 11	209.4	20.9 152037 9 HS167A19	HS167A19 Human DNA
12	205.6	20.6 181276 9 AP005130	AP005130 Homo sapi
13	205.6	20.6 181361 2 AC015571	AC015571 Homo sapi
14	205.6	20.6 183466 9 AP005241	AP005241 Homo sapi
C 15	200.8	20.1 164175 2 AC119056	AC119056 Papio anu
16	200.8	20.1 182902 9 AC092405	AC092405 Papio anu
17	200.6	20.1 198700 9 AC104317	AC104317 Homo sapi
18	200.6	20.1 198899 9 AC090192	AC090192 Homo sapi
C 19	199.8	20.0 182741 2 AC018910	AC018910 Homo sapi

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21	199.4	19.9	91842	9	AC008392	AC008392 Homo sapi
22	199.4	19.9	120426	9	HS1116H23	AL121890 Human DNA
C 23	199.4	19.9	149437	2	AC027218	AC027218 Homo sapi
C 24	199.2	19.9	81001	6	AR232007	AR232007 Sequence
C 25	199.2	19.9	81001	6	AX063464	AX063464 Sequence
C 26	199.2	19.9	81001	6	AX469876	AX469876 Sequence
C 27	199.2	19.9	113980	2	AP001540	AP001540 Homo sapi
C 28	199.2	19.9	188963	9	AC007707	AC007707 Homo sapi
29	198.8	19.9	86172	9	AY016370	AY016370 Homo sapi
C 30	198.8	19.9	154561	9	AC021355	AC021355 Homo sapi
31	198.8	19.9	164268	9	AC099332	AC099332 Homo sapi
32	198.8	19.9	173557	9	AC146142	AC146142 Pan trogl
C 33	198.8	19.9	173580	9	AC104850	AC104850 Homo sapi
C 34	198.6	19.9	28941	9	AC124902	AC124902 Homo sapi
C 35	198.6	19.9	36246	9	AC092316	AC092316 Homo sapi
C 36	198.6	19.9	46534	9	HS1057D18	AL035450 Human DNA
C 37	198.6	19.9	69912	2	AC010322	AL010322 Homo sapi
C 38	198.4	19.8	160039	9	AC106804	AC106804 Homo sapi
C 39	198.4	19.8	200838	9	AC020763	AC020763 Homo sapi
C 40	197.6	19.8	177334	9	AP006216	AP006216 Homo sapi
C 41	197.4	19.7	149136	9	AC008033	AC008033 Homo sapi
C 42	197.2	19.7	110013	2	AC046157	AC046157 Homo sapi
C 43	197.2	19.7	154616	2	AC067772	AC067772 Homo sapi
C 44	197.2	19.7	155770	2	AC092381	AC092381 Homo sapi
45	197.2	19.7	159539	9	AC096632	AC096632 Homo sapi

ALIGNMENTS

RESULT 1
LOCUS AX711964 43543 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 3 from Patent WO02062977.
ACCESSION AX711964
VERSION AX711964.1 GI:29787749
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Yan, C., Ketchum, K., di Francesco, V. and Beasley, E. M.
TITLE Human phospholipase b-like polypeptide and uses thereof
JOURNAL Patent: WO 02062977-A 3 15-AUG-2002;
PE Corporation (NY) (US)
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Location/Qualifiers
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ORIGIN			
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Qy	61	AGGCAGATTTCCAGGAGTTGGAGACACAGCTTGAGCACTTTGGTGAACCTGCTCTAC	120
Db	22111	AGGCAGATTTCCAGGAGTTGGAGACACAGCTTGAGCACTTTGGTGAACCTGCTCTAC	22170
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LOCUS	AC022076	Homo sapiens chromosome 3 clone RP11-34L7, WORKING DRAFT SEQUENCE,			
DEFINITION	AC022076	11 unordered pieces.			
ACCESSION	AC022076				
VERSION	AC022076.13	GI:20335454			
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.				
SOURCE	HTG; HTGS_PHASE1; HTGS_DRAFT.				
ORGANISM	Homo sapiens	(human)			
REFERENCE	Homo sapiens	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1	(bases 1 to 163595)			
	Murphy D.M., Adams C., Adio-Oduola B., Ali-osman F.R., Allen C., Albrooks S.L., Amarantunge H.C., Are J.R., Ayele M., Banks T., Barbacia J., Benton J., Bimage K., Blankenburg K., Bonnin D., Bouck J., Bowie S., Brileva M., Brown E., Brown M., Bryant N.P., Buhay C., Burch P., Burkett C., Burrell K.L., Byrd N.C., Carron T.F., Carter M., Cavazos S.R., Chacko J., Chavez D.,				

TITLE
JOURNAL
REFERENCE
2 (bases 1 to 163595)
Worley, K.C.
Direct Submission
Submitted (26-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 163595)
Worley, K.C.
Direct Submission
Submitted (08-JAN-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Apr 28, 2002 this sequence version replaced gi:16117882.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HAPB
Center clone name: RP11-34L7
----- Summary Statistics
Sequencing vector: M13;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 156062 bases at least Q40
Consensus quality: 159373 bases at least Q30
Consensus quality: 160990 bases at least Q20
Estimated insert size: 163913; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
consists of 11 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as

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Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@wustl.wustl.edu
 ----- Summary Statistics
 Center project name: H_NH0780J06

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenoe, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. *Genomics* 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:
 The clone sequenced to the right is AC022076. Actual start of this clone is at base position 1 of RP11-780J6; actual end is at base position 180465 of RP11-780J6.

FEATURES

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RESULT 4

AC090058/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AC090058

Homo sapiens 12 BAC RP11-112N23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.

AC090058

AC090058.21

GI:24431570

HTG.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaraturunge,H.C., Are,J.R., Ayale,M., Banks,T., Barbra,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buahy,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Emerling,S., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Han,J., Harris,C., Harris,K., Hart,M., Haviak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Ioshikhes,I., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Lead,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulewed,H., Lozado,R.J., Lu,X., Lucifera,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Marcondel,I., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Merscher,S., Metzbak,M., Miller,A., Miner,G., Miner,Z., Mitchell,T., Moncharat,K., Montgomery,K.T., Morgan,M., Morris,S., Moser,M., Neul,D., Nelson,D., Newton,J., Newton,S., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokwenkwo,S., Ogih,M., Okunou,G., Oragunye,N., Oviado,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Picken,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savary,G., Scherer,S., Scott,G., Shen,H., Shim,C., Shoonstari,N., Sisson,I., Sodergren,B., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vaquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wallington,S., Williams,G., Williamson,A., Wleciyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y.F., Zhou,J., Zorrilla,S., Zuchlerapatti,R., Weinstein,G. and Gibbs.R.

Mon Mar 28 09:43:30 2005

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REFERENCE	2 (bases 1 to 181102)	/chromosome="12"
AUTHORS	Worley K.C.	/clones="RP11-112N23"
TITLE	Direct Submission	complement(1..2004)
JOURNAL	Submitted (14-FEB-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	/note="overlaps bases 1..2000 of clone AC140061"
REFERENCE	3 (bases 1 to 181102)	/function="clone overlap"
AUTHORS	Worley K.C.	23..300
TITLE	Direct Submission	/rpt_family="AluSc"
JOURNAL	Submitted (12-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	303..337
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AUTHORS	Worley K.C.	complement(517..615)
TITLE	Direct Submission	/rpt_family="MIR"
JOURNAL	Submitted (31-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	complement(616..911)
REFERENCE	5 (bases 1 to 181102)	/rpt_family="AluSg"
AUTHORS	Worley K.C.	complement(912..1002)
TITLE	Direct Submission	/rpt_family="MIR"
JOURNAL	Submitted (12-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	1083..1241
REFERENCE	6 (bases 1 to 181102)	/rpt_family="(CA)n"
AUTHORS	Worley K.C.	complement(1433..1727)
TITLE	Direct Submission	/rpt_family="AluJb"
JOURNAL	Submitted (27-DEC-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	2153..2191
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AUTHORS	Worley K.C.	complement(2254..2548)
TITLE	Direct Submission	/rpt_family="AluSx"
JOURNAL	Submitted (31-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	2839..3102
REFERENCE	8 (bases 1 to 181102)	/rpt_family="AluJo"
AUTHORS	Worley K.C.	complement(3211..3507)
TITLE	Direct Submission	/rpt_family="AluSx"
JOURNAL	Submitted (28-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	3966..4261
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AUTHORS	Worley K.C.	4552..4747
TITLE	Direct Submission	/rpt_family="AluSg/x"
JOURNAL	Submitted (31-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	4810..4830
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AUTHORS	Worley K.C.	4855..4887
TITLE	Direct Submission	/rpt_family="(TTTTA)n"
JOURNAL	Submitted (28-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	complement(4894..5183)
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AUTHORS	Worley K.C.	complement(5184..5378)
TITLE	Direct Submission	/rpt_family="AluJo"
JOURNAL	Submitted (31-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	5379..5640
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AUTHORS	Worley K.C.	complement(5641..5742)
TITLE	Direct Submission	/rpt_family="AluJo"
JOURNAL	Submitted (28-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	complement(5852..6017)
REFERENCE	13 (bases 1 to 181102)	/rpt_family="AluSx"
AUTHORS	Worley K.C.	complement(6018..6329)
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JOURNAL	Submitted (31-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	complement(6330..6461)
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AUTHORS	Worley K.C.	complement(6530..7093)
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JOURNAL	Submitted (28-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	7096..7377
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AUTHORS	Worley K.C.	7381..7527
TITLE	Direct Submission	/rpt_family="AluSg/x"
JOURNAL	Submitted (31-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	7553..7586
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AUTHORS	Worley K.C.	complement(7607..7706)
TITLE	Direct Submission	/rpt_family="L1PA16"
JOURNAL	Submitted (28-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	7711..7844
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AUTHORS	Worley K.C.	complement(7847..8356)
TITLE	Direct Submission	/rpt_family="L1P"
JOURNAL	Submitted (31-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	8360..8420
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AUTHORS	Worley K.C.	8421..8608
TITLE	Direct Submission	/rpt_family="AluSc"
JOURNAL	Submitted (28-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	8615..8676
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AUTHORS	Worley K.C.	complement(8682..8937)
TITLE	Direct Submission	/rpt_family="AluSx"
JOURNAL	Submitted (31-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	

FEATURES
source

Location/Qualifiers
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/organism="Homo sapiens"

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:
http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht

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Matches 438; Conservative 0; Mismatches 159; Indels 34; Gaps 7;

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LOCUS BS000244 155086 bp DNA linear PRI 12-JUN-2004
DEFINITION Pan troglodytes chromosome 22 clone:PTB-070F15, map 22, complete
sequences.
ACCESSION BS000244 BA000046
VERSION BS000244.1 GI:37537511
KEYWORDS HTG.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE
1
AUTHORS The International Chimpanzee Chromosome 22 Consortium.
TITLE DNA sequence and comparative analysis of chimpanzee chromosome 22
JOURNAL Nature 429, 382-388 (2004)
REFERENCE
2 (bases 1 to 155086)
AUTHORS Teai,S., Liu,T., Wu,K., Liao,T. and Hsiao,K.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2003) Shih-Peng Teai, National Health Research
Institutes (NHRI), Division of Molecular and Genomic Medicine; 128,
Yen-Chiu-Yuan Road, Sec 2, Taipei 115, Taiwan

```

```

(E-mail:petasai@nhri.org.tw, URL:http://www.nhri.org.tw/,
Tel:886-2-28267319, Fax:886-2-28200552)
The Chimpanzee Chromosome 22 Sequencing Consortium consists of:
*Chinese National Human Genome Center at Shanghai, Shanghai, China;
*GBF, Dept. of Genome Analysis, Braunschweig, Germany; *Institute
of Molecular Biotechnology, Jena, Germany; *KRIIBB Genome Research
Center, Daejeon, Korea;
*Wax-Plant-Institute for Molecular Genetics, Berlin, Germany;
*National Institute of Genetics, Mishima, Japan;
*National Yang Ming University Genome Research Center, Taipei,
Taiwan;
*RIKEN Genomic Sciences Center, Yokohama, Japan.
Center: National Yang Ming University Genome Research Center
code: YMGC
Web site: http://genome.ym.edu.tw/
Contact: sequence@ym.edu.tw
----- Project Information
Center project name:The Chimpanzee Chromosome 22 Sequencing Project
Center clone name: HK
----- Summary Statistics
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator Big Dye and ET; 100% of reads Assembly
program: Phrap; version 0.990319
Consensus quality: 155,072 bases at least Q40
Consensus quality: 155,086 bases at least Q30
Consensus quality: 155,086 bases at least Q20
-----
This sequence was finished as follows unless otherwise noted: all
regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30);
an attempt was made to resolve all sequencing problems, such as
compressions and repeats; all regions were covered by at one
subclone or more than one M13 subclone;
and the assembly was confirmed by restriction digest.
-----
Source information:
The PTB1 chimpanzee BAC library was prepared from DNA isolated from
cultured cells established from the blood of a single male
chimpanzee.
Clones may be obtained from Asao Fujiyama and co-workers
(http://www.gsc.riken.go.jp).
VECTOR: pK3145
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Sequence Quality Assessment:
This entry has been annotated with sequence
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in
10,000 bp.
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Neighboring clones: CH251-388003(left) and PTB-059I14(right).
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Best Local Similarity 68.0%; Pred. No. 1e-47;
Matches 405; Conservative 0; Mismatches 176; Indels 15; Gaps 5;

QY 5 TTTGGCTGGTGGCTGGCTCAGCCTTAATCCAGACATTTGGGAGGCCAAGGTAGGC 64
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Web site: http://genome.ym.edu.tw/	
Contact: sequenceym.edu.tw	
----- Project Information	
Center project name: The Chimpanzee Chromosome 22 Sequencing Project	
Center clone name: HL	
----- Summary Statistics	
Sequencing vector: pUC18; 100% of reads	
Chemistry: Dye-terminator Big Dye and ET; 100% of reads Assembly	
Program: Phrap; version 0.990319	
Consensus quality: 201,270 bases at least Q40	
Consensus quality: 201,301 bases at least Q30	
Consensus quality: 201,302 bases at least Q20	

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30);	
an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at one plasmid	
subclone or more than one M13 subclone;	
and the assembly was confirmed by restriction digest.	

Source information:	
The PTB1 chimpanzee BAC library was prepared from DNA isolated from cultured cells established from the blood of a single male chimpanzee.	
Clones may be obtained from Asao Fujiyama and co-workers (http://www.gsc.riken.go.jp).	
VECTOR: pKS145	

Sequence Quality Assessment:	
This entry has been annotated with sequence estimates computed by the Phrap assembly program.	
All manually edited bases have been reduced to quality zero.	
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.	

Neighboring clones: PTB-070P15 (left) and PTB-339M13 (right).	

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Best Local Similarity 68.0%; Pred. No. 1e-47;	
Matches 405; Conservative 0; Mismatches 176; Indels 15; Gaps 5;	
Qy 5 TTTGGCTGGGTGGGTGGCTCAGCCTTAATCCAGACACTTTGGGAGGCCAAGGTAGGC 64	
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Db 30589 AGATCACTAGGTGAGGATCGAGACCATCTTGGTGAACCGTGTGAACCCCTGTCTCTAC 30648	
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Db 30649 TAAAAATACAAAAAATAATTAGCCGAGTGTGGTGGCGGCTCTATAGTCCCAGCTACTTG 30708	
Qy 179 GAAGCGTGAATGGGAGGATCACTTGGCTCAGAGGGTTGAGGCTGAGTGGAGCCGTGA 238	
Db 30709 GGAGACTGAGCGAGGAATCGCTTGAAC--CCGAGGCGGAGGTTGCGATGAGCCAAG 30767	
Qy 239 TCACACCACTACTCTCCAGCTGGGCAACAGACCCCTCTCTCAAAAAGGATACAA 298	

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180	Qy	AAGCGCTGAGATGGAGGATCAGTTGAGCTCAGAGGGGTTGAGGCTCGAGTGAGCCCGTGAT	239
9655	Db	GAGACTTGAGCGAGGAGAAATCGCTTTGAAC-CCGAGAGCGGAGGTTGAGTGAGCCCAAGAT	9713
240	Qy	CACACCACTACACTCCAGAGCTGGGCAACAGAGCAAGACCCCTGTCTCAAAAGAGATACAAT	299
9714	Db	TGTTGTCACCTTCACTCCAGCCTGGGCGATAGAGTGAGACTCCTTCTCAAAAGTTTAAAG	9773
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9774	Db	CATTTGTACAGCTGTGGAAAGCATCACTACAATCAAGATAGTGACCATATCCAGCAGGCC	9833
360	Qy	CAGGAGTTTTCTCAGGCCCCCTGGTAAATCTCTCCCTCCTGCTCCTTCTGTCGCTTACCTC	419
9834	Db	CAAAAGTGTCTTGTGTGTTCTTGGTCTCCTC-CTCTCTTCGGATCCTCTTCTGGCTTTCGCCAT	9892
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533	Qy	AAATGATTTTGGATGCAATCCAGTTATTCGGGATACCAATAGTTTCGCCCTTT	587
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AP000216 100000 bp DNA linear PRI 20-NOV-1999			
DEFINITION			
Homo sapiens genomic DNA, chromosome 21q22.3-ter, Ter region, clone f27E1-T1136, segment 2/4, complete sequence.			

REFERENCE
2 (bases 1 to 100000)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y. and Sakaki, Y.
Direct Submission
Submitted (10-MAY-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitasato Univ., 1-15-1 Kitasato, Sagami-hara, Kanagawa 228-8555,
Japan (E-mail: hattori@gsc.riken.go.jp,
URL: <http://hgp.gsc.riken.go.jp/>, Tel: 81-42-778-9923,
Fax: 81-42-778-9924)

FEATURES Location/Qualifiers
source 1..100000
FAX:81-42-778-9924)

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Matches 401	Conservative 0	Mismatches 180	Indels 14	Gaps 5

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Db 24592 TTGGCTGGGTGGTGGCTCAGGCTCTAATCCAGCACCTTTGGAGGCCCAAGTGGC 24651
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Db 24772 GAGACTGAGCAGGAGAAATCGCTTTGAC-CCGAGAGCGGAGGTTGCACTGAGCCCAAGT 24830
QY 240 CACACCACTACCTCCAGCCTGGGCAACAGAGCAAGACCTGTCTCAAAAAGATACAT 299
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Db 24891 CATTTGTACAGCTGTGAAAGACATCACTAACAATCAAGATGATGACATATCCAGACGCC 24950
QY 360 CAGAGGTTTCTCAGGCGCCCTTGGTAAATCTCTCCCTCTCTCTCTCTCTCTCTCTCTCT 419
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LOCUS Homo sapiens genomic DNA, chromosome 21q, section 104/105.
DEFINITION AP001760 AL163305 BA000005
ACCESSION AP001760.1 GI:7768687
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1
AUTHORS Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
Park H.S., Toyoda A., Iehli K., Totoki Y., Choi D.K., Soeda E.,
Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R.,
Patterson D., Reichwald K., Rump A., Schillhabel M., Schudy A.,
Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Kawasaki K.,
Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Kawasaki K.,
Asakawa S., Shintani A., Sasaki K., Nagamine K., Mitsuoyama S.,
Antonarakis S.E., Minoshima S., Shimizu N., Nordsiek G.,
Hornischer K., Barand P., Scharfe M., Schoen O., Desario A.,
Reichelt J., Kauer G., Bloeker H., Ramser J., Beck A., Klages S.,
Hennig S., Riesselmann L., Dagand E., Wehrmeyer S., Borzym K.,
Gardiner K., Nizetic D., Francis F., Lehrach H., Reinhardt R. and
Yaspo M.L.
The DNA sequence of human chromosome 21
Nature 405 (6784), 311-319 (2000)
JOURNAL
MEDLINE
PUBMED 20289799
10830953
REFERENCE
2 (bases 1 to 340000)
AUTHORS Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
Park H.S., Toyoda A., Ishii K., Totoki Y., Choi D.K., Soeda E.,
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Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R.,
Patterson D., Reichwald K., Rump A., Schillhabel M., Schudy A.,
Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Kawasaki K.,
Asakawa S., Shintani A., Sasaki K., Nagamine K., Mitsuoyama S.,
Antonarakis S.E., Minoshima S., Shimizu N., Nordsiek G.,
Hornischer K., Barand P., Scharfe M., Schoen O., Desario A.,
Reichelt J., Kauer G., Bloeker H., Ramser J., Beck A., Klages S.,
Hennig S., Riesselmann L., Dagand E., Wehrmeyer S., Borzym K.,
Gardiner K., Nizetic D., Francis F., Lehrach H., Reinhardt R. and
Yaspo M.L.

TITLE
JOURNAL

Submitted (10-APR-2000) The Chromosome 21 Mapping and Sequencing
Consortium: * RIKEN Genomic Sciences Center, Human Genome Research
Group * Institute of Molecular Biotechnology, Genome Analysis *
Keio University School of Medicine, Dept. of Molecular Biology *
Genetics (addresses see below)

COMMENT

On May 30, 2000 this sequence and sequencing consortium consisting of
* RIKEN Genomic Sciences Center, Human Genome Research Group, *
Sagamihara 228-8555, Japan, *
* e-mail: hattori@gs.riken.go.jp/
* URL: http://hgp.gsc.riken.go.jp/
and
* Institute of Molecular Biotechnology, Genome Analysis, *
Beutenbergstrasse 11, D-07745 Jena, Germany,
* e-mail: gscj-submit@genome.imb-jena.de
* URL: http://genome.imb-jena.de/
and
* Keio University School of Medicine, Molecular Biology, * Tokyo
160-8582, Japan,
* e-mail: nshimizue@dm-b.med.keio.ac.jp/
* URL: http://www.dmb.med.keio.ac.jp/
and
* GSF, Dept. of Genome Analysis,
* Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e-mail:
info.genome@gsf.de
* URL: http://genome.gsf.de/
and
* Max-planck Institute for Molecular Genetics,
* Innestrasse 73, D-14195 Berlin, Germany,
* e-mail: info-chr21@molgen.mpg.de/
* URL: http://chr21.rz-berlin.mpg.de/
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Matches 401; Conservative 0; Mismatches 180; Indels 14; Gaps 5;
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Db 184051 TTTCGCTGGGCGGTGGCTCACACCTGTAATCCAGACACTTTGGAGGCTGAGCGCGC 184110
Qy 65 AGA---TTGCCCGAGGAGTTGGAGACCACTGTGAGCACTTTGGTGAACCTGTCTCTAC 120
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Qy 180 AAGCTGAGATGGGAGGATCACTTGAGCTAGAGGGTTGAGGCTGAGTGCAGTGCAGCGTAT 239
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Db 184469 ACCTTCAGGAGCACCAGATTACTTCTGTCTACTATAGATAGATTTCTCTAGA 184528
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RESULT 10
AL589987/c 143770 bp DNA linear PRI 22-MAY-2002
LOCUS

Human DNA sequence from clone RP11-364B14 on chromosome X, complete sequence.

DEFINITION
ACCESSION AL589987
VERSION AL589987.25 GI:21211755
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1. (bases 1 to 143770)
AUTHORS Ashwell R.
TITLE Direct Submission
JOURNAL Submitted (21-MAY-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT On May 25, 2002 this sequence version replaced gi:17154304. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/ChrX> RP11-364B14 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACes.6.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
/clone="RP11-364B14"
/clone_lib="RPCI-11.2"

FEATURES
source

ORIGIN
Query Match 21.4%; Score 213.8; DB 9; Length 143770;
Best Local Similarity 68.2%; Pred. No. 1.4e-42;
Matches 436; Conservative 0; Mismatches 152; Indels 51; Gaps 8;
QY 9 GCTGGGTGGCGTCAACCTCTAATCCAGCACTTTGGGAGGCCAAGGTAGGCAGAT 68
DB 41455 GCCGGGAACAGTGGCTCATCTATATCCAGCACTGTGGAGGCCAAGGTAGGCAGAT 41396
QY 69 T-----GCCAGAGTTGAGACCACTGTGAGCAACTTGGTGAACCCCTGTCTTACCA 122
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DB 41335 AAAATGAATAAATAATTAGTCAGGTATGGTGTGTGCGCTACAGCCCAAGCTACTAGGG 41276
QY 191 AGGCTGAGATGGGAGGATCACTTCAGCTCAGAGGGGTTGAGGCTGCAAGTGCAGCCGTGATC 240
DB 41275 AGGCTGAGTGGGAGGATGTCGGAGC-CTGGGAGGTCAAGTCTGCAGTGAGCCAGATC 41217
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QY 333 CAAGATGAAATGTTTATCACCCAGAGGTTTCTCAGGGCCCTTGGTAATCTCTC 392
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Db 40858 TATCTGATTTCTTAGTTTCTTCTCTCTGAGTATTTTATGCTGAGT 40820

RESULT 11
HS167A19/c
LOCUS Human DNA sequence from clone RP1-167A19 on chromosome 1p32.1-33,
DEFINITION complete sequence.
ACCESSION AL031427
VERSION AL031427.15 GI:4835258
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1. (bases 1 to 152037)
AUTHORS Hall, R.
TITLE Direct Submission
JOURNAL Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT On May 14, 1999 this sequence version replaced gi:4808231.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human


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Db      78933 AAACAAAAAACTACTGCAAGCTTTTCACAA 78962

RESULT 14
LOCUS   AP005241
DEFINITION Homo sapiens genomic DNA, chromosome 18 clone:RP11-502P1, complete
sequence.
ACCESSION AP005241
VERSION   AP005241.4
KEYWORDS HTG.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

REFERENCE
AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE     Homo sapiens genomic DNA
JOURNAL   Published Only in Database (2002)
REFERENCE 2 (bases 1 to 183466)
AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE     Direct Submission
JOURNAL   Submitted (22-MAY-2002) Maehira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Sushiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsr.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT   On Jun 13, 2003 this sequence version replaced gi:29243375.
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Best Local Similarity 78.8%; Pred. No. 1.6e-40;
Matches 260; Conservative 0; Mismatches 64; Indels 6; Gaps 1;

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Db      157410 TTTGGCTGGGTGAGTGCTCATGCTGTATCCAGACACTTGGAGGCTGAGCGGGC 157469

Qy      65 AGATT-----GCCAGAGTTGGAGACCACTGTGAGCAACTTGGTGAACCCCTGTCTT 118
Db      157470 AGACTGCTTGAGCCCGAGGAGTTCGAGACCGCTGGGCAACATGCTGAACCCATTGTCT 157529

Qy      119 ACCAAATAACAAAATATACCGGGATGTGCGATGACCTGTAGTCCAGTACTCG 178
Db      157530 ACCAAATAACAAAATATACCGGGATGTGCGATGACCTGTAGTCCAGTACTCG 157589

Qy      179 GAAGGCTGAGATGGAGGATCACTTGAGCTCAGAGGGGTTGAGGCTGAGTGGCGGTGA 238
Db      157590 GGAGGCTGAGTGGAGGATGCTTGAGCCGGGAGCGGAGGTGCATGACTGTGA 157649

Qy      239 TCACACCACTACATCCAGCTGGGCAACAGAGCAAGACCTGTCTCAAAAGATACAA 298
Db      157650 TTGCACCACTGCACTCCAGCTGGGTGACAGTAAAGACAGTCTCAAAACAAACAA 157709

Qy      299 TTTAACATTGACTGTGAATCATCACCA 328
Db      157710 AAACAAAAAACTACTGCAAGCTTTTCACAA 157739

RESULT 15
LOCUS   AC119056/c
DEFINITION Papio anubis clone RP41-356H11, WORKING DRAFT SEQUENCE, 10 ordered

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ACCESSION AC119056
VERSION   AC119056.4
KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT.
SOURCE    Papio anubis (Olive baboon)
ORGANISM  Papio anubis

REFERENCE
AUTHORS   Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Carriaga,K., Coleman,B., Dietrich,N.L., Engle,J., Granite,S.,
Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L.,
Idol,J.R., Karlins,E., Laric,P., Lee-Lin,S.-Q., Legaspi,R.,
Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masiello,C., Maskeri,B.,
Mastrian,S.D., McCloskey,J.C., McDowell,J., Paquinigan,C.,
Pearson,R., Portnoy,M.E., Prasad,A., Reddix-Dugue,N., Schandler,K.,
Schueler,M.G., Sison,C., Stantripop,S., Thomas,J.W., Thomas,P.J.,
Touchman,J.W., Vogt,J.L., Walker,M., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
TITLE     NISC Comparative Sequencing Initiative
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 164175)
AUTHORS   Green,E.D.
TITLE     Direct Submission
JOURNAL   Submitted (24-APR-2002) NIH Intramural Sequencing Center, 8717
Grovenmont Circle, Gaithersburg, MD 20877, USA
REFERENCE 3 (bases 1 to 164175)
AUTHORS   Green,E.D.
TITLE     Direct Submission
JOURNAL   Submitted (03-DEC-2002) NIH Intramural Sequencing Center, 8717
Grovenmont Circle, Gaithersburg, MD 20877, USA
On Dec 3, 2002 this sequence version replaced gi:23237967.
COMMENT   ----- NISC Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.zoo@nhgri.nih.gov
----- Project Information
Center project name: det
Center clone name: 356H11

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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

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----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 162540 bases at least Q40
Consensus quality: 162989 bases at least Q30
Consensus quality: 163178 bases at least Q20
Insert size: 140000; agarose-fp
Insert size: 163275; sum-of-contigs
Quality coverage: 23.62x in Q20 bases; agarose-fp
Quality coverage: 20.25x in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 26, 2005, 08:45:20 ; Search time 520.763 Seconds
(without alignments)
11367.434 Million cell updates/sec

Title: US-09-778-961-3_COPY_22051_23050

Perfect score: 1000

Sequence: 1 ataatttggtgggtgcggt.....agggaagtcctcagagggga 1000

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1000	100.0	43543	6	AbQ82235 Human pho
2	199.2	19.9	10316	4	Aak89399 Human dig
3	199.2	19.9	81001	4	Aaf30035 Human apo
4	199.2	19.9	18971	12	AdL08108 Human gen
5	197	19.7	154681	10	AdL13861 Osteoarth
6	194.4	19.4	4583	4	Aak67070 Human imm
7	194.2	19.4	145985	12	AdQ97164 Human can
8	193.4	19.3	6268	4	AAS32707 Human gen
9	193	19.3	19183	4	Aak64938 Human imm
10	193	19.3	19183	4	AAL36434 Human mus
11	193	19.3	19183	8	ADX59422 CDNA enco
12	193	19.3	19183	12	AdJ30172 Human mus
13	192.8	19.3	261817	11	Acn45182 Human gen
14	192.6	19.3	7385	4	Aah72843 Human cer
15	192.6	19.3	24961	13	AdS36469 Human aut
16	191.8	19.2	109906	6	AbK94411 DNA encod
17	191.8	19.2	109906	12	AdL08112 Human gen
18	191	19.1	7588	4	AaI62714 Human bre
19	191	19.1	7588	4	AaL07036 Human rep
20	191	19.1	20001	13	Acn37208 Human per

ALIGNMENTS

RESULT 1

ABQ82235

ID ABQ82235 standard; DNA; 43543 BP.

XX AC ABQ82235;

XX DT 16-DEC-2002 (first entry)

XX DE Human phospholipase protein encoding DNA SEQ ID NO:3.

XX KW Human; phospholipase; enzyme; chromosome 2; gene; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

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23	190.6	19.1	19866	8	ABZ74457	Abz74457 Secreted
24	190.6	19.1	19866	8	ABX60510	Abx60510 cDNA enco
25	190.6	19.1	19866	10	ABZ68004	Abz68004 Human sec
26	190.6	19.1	19866	12	ADJ31260	Adj31260 Human mus
27	190.2	19.0	99014	6	ABN96931	Abn96931 Gene #342
28	189.8	19.0	238484	11	ACN44210	Acn44210 Human gen
29	189.6	19.0	120670	12	ADQ59167	Adq59167 MSI-H car
30	189.4	18.9	6871	4	AAS32589	Aas32589 Human gen
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32	189	18.9	63686	11	ACN44158	Acn44158 Human gen
33	188.8	18.9	16854	5	AAS29953	Aas29953 Human lun
34	188.8	18.9	16854	10	ADB33290	Adb33290 Human nov
35	188.8	18.9	76201	12	ADJ62814	Adj62814 Human cDN
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38	188.6	18.9	110000	10	ADG70184_2	Continuation (3 of
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us-09-778-961-3_copy_22051_23050.rng

Mon Mar 28 09:43:30 2005

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Best Local Similarity 100.0%; Pred. No. 9.7e-251;			
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Db	22051	ATAATTTGGCTGGGTGGGTGGCTCAGCCCTCTAATCCAGCACCTTTGGGAGGCAAGGT	22110
Qy	61	AGGCAGATTGCCAGGAGTTGGAGACCACTCTGAGCAACTTGGTGAACCCCTGCTCTAC	120
Db	22111	AGGCAGATTGCCAGGAGTTGGAGACCACTCTGAGCAACTTGGTGAACCCCTGCTCTAC	22170
Qy	121	CAAAATAACAAAAATTAGCCGGGCATGGTGGCATGGACCTGTAGTCCAGCTACTCGGA	180
Db	22171	CAAAATAACAAAAATTAGCCGGGCATGGTGGCATGGACCTGTAGTCCAGCTACTCGGA	22230
Qy	181	AGGCTGAGATGGGAGGATCACTTGAGCTCAGAGGGGTTGAGGCTGCAGTGGCGTGAATC	240
Db	22231	AGGCTGAGATGGGAGGATCACTTGAGCTCAGAGGGGTTGAGGCTGCAGTGGCGTGAATC	22290
Qy	241	ACACCACCTACACTCCAGCTGGGCAACAGACAGACCCCTGCTCAAAAAGGATACAAAT	300
Db	22291	ACACCACCTACACTCCAGCTGGGCAACAGACAGACCCCTGCTCAAAAAGGATACAAAT	22350
Qy	301	TAACTTTGACCTGTGAATCATCACCACATCAAGATGAAAAATGTGTTTATCACCCAC	360
Db	22351	TAACTTTGACCTGTGAATCATCACCACATCAAGATGAAAAATGTGTTTATCACCCAC	22410
Qy	361	AGGAGTTTCTCAGGCCCTTGTTAACTCTCCCTCTGCTCCCTTCTGCTCCCTACCTCA	420
Db	22411	AGGAGTTTCTCAGGCCCTTGTTAACTCTCCCTCTGCTCCCTTCTGCTCCCTACCTCA	22470
Qy	421	CACCCAGGCAACCACTAACCTCTTTCCATCAATAGATTAGTTGCAATTTTAAAAA	480
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Qy	481	TTTTATATAATGGGATCAAGAGTATATATCTTTTATCTGACTTATTAGCAAAATGAT	540
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Qy	541	TTTGGGATGCATCATGTTATTTCGGTATACCAATAGTTGCTCCCTTTTATGCGTGAATG	600
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Qy	601	TAGTGTTCGGTTGGCATTCATATCGCTCATCCAGAACCAAAATGTTGTTTATTTA	660
Db	22651	TAGTGTTCGGTTGGCATTCATATCGCTCATCCAGAACCAAAATGTTGTTTATTTA	22710
Qy	661	TGGCAGACATCAGGGGATGAAGGAGAACTAATCTGTCCATCTCTGGTTTATTCGAGAGG	720
Db	22711	TGGCAGACATCAGGGGATGAAGGAGAACTAATCTGTCCATCTCTGGTTTATTCGAGAGG	22770
Qy	721	GAGAAAAAATAGTAGGAGATGGGAAATGGTCGGAAATCTAAGTAACACAGAAAAAG	780
Db	22771	GAGAAAAAATAGTAGGAGATGGGAAATGGTCGGGAAATCTAAGTAACACAGAAAAAG	22830
Qy	781	AAAAACAAAAGGATTAAGGAGCAGAGCAGGCTTAGAAGTAAAGGTTAAAGGAGTCA	840
Db	22831	AAAAACAAAAGGATTAAGGAGCAGAGCAGGCTTAGAAGTAAAGGTTAAAGGAGTCA	22890

Qy	841	TTAAGCCTGGAAAGGAGAAAACTGAGGATAAATTGTGAGCTGTGACTTTTCTCAAATATA	900
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AC	AAK89399;		
XX	05-NOV-2001 (first entry)		
DT	Human digestive system antigen genomic sequence SEQ ID NO: 2975.		
DE	Human; digestive system antigen; gene therapy; cancer; appendicitis;		
XX	ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;		
KW	digestive system disorder; Meckel's diverticulum; ds.		
KW	Homo sapiens.		
XX	WO200155314-A2.		
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XX	17-JAN-2001; 2001WO-US001324.		
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PR 17-NOV-2000; 2000US-0249300P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX
XX WPI; 2001-502630/55.
DR
XX
XX Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognosing disorders of the
PT digestive system, particularly cancer and cancer metastases.
XX
XX Disclosure; SEQ ID NO 2975; 986pp; English.
PS
XX
XX The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a genomic DNA fragment
CC encoding a digestive system antigen of the invention
XX
XX Sequence 10316 BP; 2525 A; 2093 C; 2534 G; 3164 T; 0 U; 0 Other;
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Best Local Similarity 77.5%; Pred. No. 2.4e-41;
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6240 AGGCAGATCAGAGGTTCAGAGTTCAGAGCAGCTGCGCCACATATGTAACCCCTGTCT 6181
117 CTACCAAAATACAAAAAATTAGCCGGGATGGTGGCATGGAGCTGTAGTCCAGCTACT 176
6180 CTACTAAATACAAAAAATTAGCCAGGCGTGGTGGTGGTCTGTAAATCCAGCTACT 6121
177 CGGAAGGCTGAGATGGGAGATCACTTGAGCTCAGAGGGGTTCAGCTGCAGTGAGCCGT 236
6120 CGGAGGCTGAGGAGCAGAAATCGCATGAAC-CCGAGGAGCAGAGTTTCAGTGAGCCGA 6062
237 GATCACACCACTACCTCCAGCCTGGGCAACAGAGCAAGACCCCTGTCTCAAAAGGATAC 296
6061 GATCAGCCCACTGCATCCAGCCTGGGCAACAGAGCAAGACTCTGTCTCCAAAAAATAA 6002

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AC AAF30035;
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XX
XX 23-APR-2001 (first entry)
XX
XX Human apolipoprotein A-IV-related protein (AA4RP) gene.
XX
XX Apolipoprotein A-IV-related protein; AARPP; human; biallelic marker;
KW lipid metabolism; liver related disorder; obesity; diabetes;
KW coronary heart disease; diagnosis; gene therapy; chromosome 11; ds.
XX
XX Homo sapiens.
XX
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PI Jones KA, Schafer A;
XX WPI; 2003-559141/52.
XX
PT Determining susceptibility of an individual to joint space narrowing,
PT osteophyte development and/or joint pain comprises identifying whether
PT the individual has at least one polymorphism in a polynucleotide encoding
PT a protein.
XX
PS Disclosure; SEQ ID NO 393; 297pp; English.
XX
CC The invention relates to a method of determining susceptibility of an
CC individual to joint space narrowing and/or osteophyte development and/or
CC joint pain comprising identifying whether the individual has at least one
CC polymorphism in a polynucleotide encoding at least one of the protein
CC listed in the specification. The methods, composition and agent are
CC useful for modulating the susceptibility of an individual to joint space
CC narrowing and/or osteophyte development and/or joint pain that is
CC associated with a disease, preferably osteoarthritis. The cell line and
CC the non-human animal are useful for screening for an agent for diagnosing
CC an individual having susceptibility to joint space narrowing and/or
CC osteophyte development and/or joint pain. This sequence corresponds to
CC the polynucleotide encoding a protein listed in the specification. (Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences).
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SQ Sequence 154681 BP; 41177 Å; 36356 C; 36934 G; 40214 T; 0 U; 0 Other;

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Best Local Similarity 84.1%; Pred. No. 2.7e-40;
Matches 248; Conservative 0; Mismatches 40; Indels 7; Gaps 2;
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RESULT 6
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XX
DT 06-NOV-2001 (first entry)
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DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21882.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytosolic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX

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Mon Mar 28 09:43:30 2005

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